

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2004, 16:17:09 , Search time 3726 Seconds
(without alignments)
6718.759 Million cell updates/sec

Title: US-09-976-673-11

Perfect score: 687

Sequence: 1 atggtgagcgcgcgtgaa.....tgccgagaaggccaactga 687

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	99.4	14.5	550	5	BQ551001	BQ551001 H4006G01-5
2	71	10.3	645	1	AI389106	AI389106 GH20192.5
3	68.6	10.0	869	7	CK159167	CK159167 FGAS04056
4	67.6	9.8	639	1	AJ615477	AJ615477 AJ615477
5	67.4	9.8	675	4	BI382638	BI382638 BFLG2_000
6	66.8	9.7	944	9	CG649516	CG649516 OGLCL15TH
7	66.4	9.7	700	7	CF864358	CF864358 p8ZS009XP
8	65.8	9.6	624	8	B422085	B422085 i49qd07.b
9	65.8	9.6	982	8	CC424389	CC424389 PUHNS3TB
10	65.2	9.5	794	6	CB651092	CB651092 OSJNEB150
11	64.8	9.4	697	5	BU626888	BU626888 UI-H-FTO-
12	64.6	9.4	821	7	CK199961	CK199961 FGAS00846
13	64.2	9.3	613	4	BI386976	BI386976 BFL26_001
14	64.2	9.3	643	4	BI386699	BI386699 BFL26_001
15	64	9.3	681	9	CNS02E0D	AL193990 Tetradon
16	64	9.3	688	9	C0303305	CG030305 PUFN30TD
17	63.8	9.3	411	2	BF201975	BF201975 WHE1759-1
18	63.8	9.3	600	2	BE417750	BE417750 MUG024.B0
19	63.8	9.3	772	5	B0752733	B0752733 WHE4118.E
20	63.6	9.3	872	8	CC413363	CC413363 PUHPU48TD
21	63.6	9.3	955	9	CG365299	CG365299 OGWT62TV
22	63.4	9.2	925	9	CNS0091P	AL053013 Drosophila
23	62.8	9.1	1006	9	CC719047	CC719047 OGULN81TV
24	62.6	9.1	599	1	AI832082	AI832082 tdi2c04.x

25	62.6	9.1	689	4	BI380055	BI380055 BFLG1_001
26	62.4	9.1	1036	7	CK162903	CK162903 FGAS01551
27	62.2	9.1	638	4	BJ269933	BJ269933 BJ269933
28	62.2	9.1	742	6	CB649099	CB649099 OSJNEB12N
29	62.2	9.1	780	7	CF554490	CF554490 GGW74 Inf
30	62	9.0	786	6	CB646357	CB646357 OSJNEB08M
31	61.8	9.0	557	4	BJ233355	BJ233355 BJ233355
32	61.6	9.0	590	6	CA030137	CA030137 HK06D04F
33	61.4	8.9	540	4	BM135283	BM135283 WHE0498.B
34	61.4	8.9	635	6	CA254345	CA254345 SCBFFL411
35	61.2	8.9	724	7	CF871694	CF871694 trico28xf
36	61.2	8.9	739	6	CB645917	CB645917 OSJNEB07P
37	61.2	8.9	777	6	CB901927	CB901927 trico28xf
38	61	8.9	571	4	BI387406	BI387406 BFL26_002
39	61	8.9	629	1	ABI18745	ABI18745 ABI18745
40	61	8.9	661	4	BI385436	BI385436 BFL26_000
41	61	8.9	687	4	BI387917	BI387917 BFL26_002
42	61	8.9	813	6	CB657967	CB657967 OSJNEC13K
43	60.8	8.9	502	4	BI135401	BI135401 GHRM115.6
44	60.6	8.8	559	7	CF847678	CF847678 PSMA002XB
45	60.6	8.8	759	8	BZ577913	BZ577913 msh2_5633

ALIGNMENTS

RESULT 1
BQ551001
LOCUS
DEFINITION H4006G01-5 NIA Mouse 7.4K cDNA clone set Mus musculus cDNA clone
H4006G01 5', mRNA sequence.
ACCESSION BQ551001
VERSION BQ551001.1 GI:21451887
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
1 (bases 1 to 550)
AUTHORS VanBuren,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G.,
Martini,P.R., Stagg,C.A., Bassey,U., Aiba,K., Hamarani,T.,
Kargul,G.J., Luo,A.G., Kelso,J., Hide,W. and Ko,M.S.H.,
TITLE Assembly, verification, and initial annotation of NIA 7.4K mouse
cDNA clone set
JOURNAL Genome Res. 12 (12), 1999-2003 (2002)
MEDLINE 22354164
PUBMED 12456305
COMMENT Other ESTs: H4006G01-3
Contact: Yong Qian
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://igsun.grc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
Place: H4006 row: G column: 01
Seq primer: -21M13 Reverse
High quality sequence stop: 550
POLYA=No.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="niaEST:H4006G01-5"
/db_xref="taxon:10090"
/clone="H4006G01"
/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 7,407 clones from more

than 20 cDNA libraries."

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ORIGIN
Query Match      14.5%; Score 99.4; DB 5; Length 550;
Best Local Similarity 55.3%; Pred. No. 2e-10;
Matches 215; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 13 CTGCTGAAGAGATATCGCATCAAGATGTACATGAGGGGACCGGTGAACGGCCACTAC 72
Db 159 CTGTTTCAACGGGGTGTGTCCTATCCTGTCGAGCTGACGGCGGACGTAAACGGCCCAAG 218
QY 73 TTCAGTTCGAGGGGAGGGGAGCGCAACCCCTTCGCCGACCCACGACATGAGAATC 132
Db 219 TTCAGCTGTCCGGGAGGGGAGGGGATGCCACCTACGGCAAGCTGACCTTGAGTTC 278
QY 133 CACGTGACCGAGGGC---GCCCCCTTCGCCCTTCGACATPCCTGGGCCCTCGTGC 189
Db 279 ATCTGCACACCGGCAAGCTGCCGTGCTGGGCCACCTCCTGTCGACCACTGACCTAC 338
QY 190 GAGTACGACAGGAGCTTGTGTACACACACCGCCGAGATCCCGGACTTCTTCAAGCAG 249
Db 339 GCGGTGACGTCTTCAGCCGCTACCCCGACACAGTGAAGCAGACGACTTCTTCAAGTCC 398
QY 250 AGCTTCCCGGAGGGCTTCACCTGGGAGAGAACCAACCACTACGAGGACGGCGCATCTG 309
Db 399 GCCATGCCGGAAGGCTACGTCCAGGAGCGCAACCATCTTCTTCAAGGACGACGGCACTAC 458
QY 310 ACCGCCACAGGACACCAAGCTGAGGGGCACTGCTGATCTACAAGGTGAAGTGCAC 369
Db 459 AAGACCCCGCGGAGGTGAAGTTGAGGGGACACCCCTGGTGAACCCGATCGAGCTGAAG 518
QY 370 GGCACCAACTTCCCGCGGACGCGCCCGT 398
Db 519 GGCATCGACTTCAAGGAGGACGGCAACAT 547

RESULT 2
LOCUS      AI389106
DEFINITION GH20192.5prime GH Drosophila melanogaster head pOT2 Drosophila
            melanogaster cDNA clone GH20192 5, mRNA sequence.
ACCESSION  AI389106
VERSION     AI389106.2 GI:13758704
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 645)
AUTHORS     Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
JOURNAL     BDGP/HMI Drosophila EST Project
COMMENT     On Jan 28, 1999 this sequence version replaced gi:4203117.
            Other ESTs: GH20192.3prime
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: GH 201 row: H column: 8
            High quality sequence stop: 627
            POLYA=No.
            Location/Qualifiers
            1..645
            /organism="Drosophila melanogaster"
            /mol_type="mRNA"
            /db_xref="taxon:7227"
            /clone="GH20192"
            /sex="male and female"
            /dev_stage="adult"

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/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."

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ORIGIN
Query Match      10.3%; Score 71; DB 1; Length 645;
Best Local Similarity 48.6%; Pred. No. 0.00015;
Matches 194; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 62 ACGGCCACTACTTCAAGTGCAGGGCGAGGGCGACGGCAACCCCTTCGCCGACCCAGA 121
Db 200 ACGACCACTCCACCATGTGCTAGGGAACACGACGACCAACAGTGTCCCTTACTACCA 259
QY 122 GATGAGAAATCACGTGACCGAGGGGCGCCCTTCGCCCTTCGCATCTCGACATCTGGCC 181
Db 260 ACAACACCAACAGTGTTCCTCCCACTACCACTACCACTACCACTACCACTACCACTAC 319
QY 182 CTTGCTGCGAGTACCGGACGAGGACCTTCTGTCACCAACCACTACCACTACCACTACCA 241
Db 320 ACCACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACT 379
QY 242 TCAACAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACCACTACGAGGACGGCG 301
Db 380 CCGACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCACTACTACT 439
QY 302 GCATCCTGACCGCCCAACGAGGACACGAGCTTGGAGGGCACTGCTGATCTACAAGTGA 361
Db 440 ACNACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 499
QY 362 AGGTCCACGGCACCAACTTCCCGCGGACGGCCCGTGTGATGAAGACGAGGCGGCT 421
Db 500 ACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 559
QY 422 GGGAGCCCGACGACGAGGTGTGTCACCCCGAGAGCGCG 460
Db 560 ACAACACCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598

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RESULT 3
LOCUS      CK159167/c
DEFINITION FGAS040564 Triticum aestivum FGAS: TaLts Triticum aestivum cDNA,
            mRNA sequence.
ACCESSION  CK159167
VERSION     CK159167.1 GI:38985053
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 869)
AUTHORS     Allard,P., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
            Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
            Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
            Penniket,C., Roach,J.L. and Sarhan,F.
            Functional Genomics of Abiotic Stress In Wheat and Canola Crops
            Unpublished (2003)
            Contact: Wm L Crosby
            Bioinformatics
            University of Saskatchewan, Department of Computer Science
            1C101 Engineering Building, 57 Campus Drive, Saskatoon,
            Saskatchewan, S7N 5A9, Canada
            Tel: 306 966 1769
            Fax: 306 966 2033
            Email: fgas\_est@cs.usask.ca
            This sequence is the direct result of the base calling software
            Phred (default parameters). It is the raw base calls. To aid in the
            identification of the high quality insert the software Lucy
            (default parameters) has been run on this sequence. Lucy identified
            the region [128,636].

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FEATURES
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        /organism="Triticum aestivum"
        /mol_type="mRNA"
        /cultivar="Wheat line PI 178383"
        /db_xref="taxon:4565"
        /lab_host="DHS alpha"
        /note="Organ: Crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H)(driver). Modified Smart cDNA (Clontech)/priming and non-directional cloning"
ORIGIN
  Query Match      10.0%; Score 68.6; DB 7; Length 869;
  Best Local Similarity 44.2%; Pred. No. 0.00048;
  Matches 284; Conservative 0; Mismatches 359; Indels 0; Gaps 0;
  QY 24 GAGTATGGCGATCAAGATGTCATGGAGGGGCAACCGTGAAGGGCCACTACTTCAAGTCCGA 83
  Db |||||
  QY 807 GAGGATCAACCAACGAGGACGAGAAACCAACCAACCAACCAACCAACCAACCAACCAACGCGA 748
  Db |||||
  QY 84 GGGGAGGGGACGCGCAACCCCTTCGGCGGCGGACCCAGAGATGATCCACGTGACCGA 143
  Db |||||
  QY 747 CACAACGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAA 688
  QY 144 GGGGCGCCCCCTGCGCTTCGCTTCGACATCTCGGCCCTTCGTGCGAGTACGGGAGCAG 203
  Db |||||
  QY 687 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAA 628
  QY 204 GACCTTGTGACCAACCAACCGCGGAGATCCCGGACTTCTTCAAGCAGAGCTTCCCGGAGG 263
  Db |||||
  QY 627 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAA 568
  QY 264 CTTCACTGGGAGAGAACCAACCACTACGAGAGCGGGGATCTGACCGCCGCCACCAAGGA 323
  Db |||||
  QY 567 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAA 508
  QY 324 CACAGCGCTGGAGGGCACTGCTCTTCAAGGTGAAGGTGACGGCACCACCTTCCC 383
  Db |||||
  QY 507 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAA 448
  QY 384 CGCGAGCGCCCTGTGATGAAGAACAAAGAGCGGGGTGGGAGCCCGACGACCGAGGTGT 443
  Db |||||
  QY 447 CAACAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 388
  QY 444 GTACCCCGAGAAACCGGCTGTGTGCGCCCGGAACGTGATGCGCTGAAGGTGGGCGGACG 503
  Db |||||
  QY 387 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACGAA 328
  QY 504 GCACCTGATCTGCCACCACTACACCACTACCGGAGCAAGAGCCGTGCGCGCCCTGAC 563
  Db |||||
  QY 327 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAA 268
  QY 564 CATGCCCGGCTTCCACTTCAACCGACATCCGGCTCCAGATGCTGGGAAGAGGAGGACGA 623
  Db |||||
  QY 267 CAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACGAA 208
  QY 624 GTACTTCGAGCTGTACGAGGCGCAGCTGGCCCGGTACAGGAC 666
  Db |||||
  QY 207 CGACAACGACGTCAACGATTAACACGACGACCAACCAACGACCAAC 165
  RESULT 4
  AJ615477 639 bp mRNA linear EST 11-DEC-2003
  LOCUS
  DEFINITION
    AJ615477 Triticum turgidum subsp. durum etiolated seedling 20 day
    Triticum turgidum subsp. durum cDNA clone 11702R, mRNA sequence.
  ACCESSION
    AJ615477
  VERSION
    AJ615477.1 GI:39732404
  KEYWORDS
    Triticum turgidum subsp. durum (durum wheat)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Poaceae; Triticeae; Triticum.
  Cifarelli,R.A., D'Onofrio,O. and Lauria,G.
  Expressed Sequences Tags (ESTs) library from totipotent cDNA of
  durum wheat
  Unpublished (2003)
  Contact: Cifarelli RA
  Biotechnology
  Metapontum Agrobiotus
  S.S. Jonica 106 km 448.2, 75010 Metaponto (MT), Italy.
  FEATURES
    Location/Qualifiers
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        /organism="Triticum turgidum subsp. durum"
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        /cultivar="Ofanto"
        /sub_species="durum"
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        /clone="11702R"
        /tissue_type="etiolated seedling"
        /dev_stage="20 day"
        /clone_lib="Triticum turgidum subsp. durum etiolated
        seedling 20 day"
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    Best Local Similarity 52.9%; Pred. No. 0.00077;
    Matches 145; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
    QY 58 GTGAACGGCCACTACTTCAAGTTCGAGGGGCGGAGGCGGCAACCCCTTGGCCGGCACC 117
    Db |||||
    QY 294 GTGCTGGGGCTCAGCAAGAAGTGCCTGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 353
    QY 118 CAGAGCATGAGAATCCAGTACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 177
    Db |||||
    QY 354 CTCGGGATCAAGTTCAAGTTCACCGCGCCATGAACCTCCCTCCGCTGCAACATCCCG 413
    QY 178 GCCCGCTGTGCGAGTACGGCAGGAGGACCTTGTGACCAACACCGCGGAGATCCCGGAC 237
    Db |||||
    QY 414 GCCACCTTTCGAGTTCGCGGAGGCTTCCCGAGGGCTTCCCTGGGAGAGACCAACCTACGAGGAC 473
    QY 238 TTCTTCAAGCAGAGCTTCCCGAGGGCTTCCCTGGGAGAGACCAACCTACGAGGAC 297
    Db |||||
    QY 474 ATCTTCAAGCAGTACGGGATCGAGCAGGAGGCGGCAAGACCGCGGCGGCGGCGGCGGCGG 533
    RESULT 5
    BI382638 675 bp mRNA linear EST 26-AUG-2003
    BFLG2_000815 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG
    or MPWGp498) Branchiostoma floridae cDNA clone MPWGp498F0258 5',
    mRNA sequence.
  ACCESSION
    BI382638
  VERSION
    BI382638.1 GI:30917704
  KEYWORDS
    EST.
  SOURCE
    Branchiostoma floridae (Florida lancelet)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
    Branchiostoma.
  REFERENCE
    1 (bases 1 to 675)
    Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J.,
    Herwig,R., Vingron,M. and Lehrach,H.
    New evidence for genome-wide duplications at the origin of
    vertebrates using an amphioxus gene set and completed animal
```

Genomes
 Journal Res. 13 (6A), 1056-1066 (2003)
 MEDLINE
 22683279
 PUBMED
 12799346
 COMMENT
 Contact: Panopoulou G
 Laboratory 145, dept.Lehrach
 Max-Planck-Institut fuer Molekulare Genetik
 Innestr.63-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1235
 Fax: +49 30 8413 1128
 Email: panopoul@molgen.mpg.de
 The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 smer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>
 Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.rzpd.de>)
 PCR Primers
 FORWARD: 5' GCGGATCTTACACTTTATGCTTCGGGCTCG 3' (M13RSP)
 BACKWARD: 5' GCTATTACCCAGCTGGCAAGAGGAGGTG 3' (M13FSP)
 Insert Length: 1 Std Error: 0.00
 Seq primer: 5'-CCGGTCCGGAATCCCGGGT-3' pSport3/86
 High quality sequence stop: 675.
 Location/Qualifiers
 1. .675
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 /mol_type="mRNA"
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 /clone="MPMGp498F0258"
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 /lab_host="E.coli, XL1 blue"
 /clone_lib="Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGP498)"
 /notes="vector: pSport1; Site 1: SalI, KpnI, EcoRI (5') ; Site_2: NotI, BamHI, HindIII (3') ; OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGATAGTTCATGATCCAGCGCGCCC (T)15-3' and a SalI 5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
 ORIGIN
 Query Match 9.8%; Score 67.4; DB 4; Length 675;
 Best Local Similarity 48.1%; Pred.No. 0.00084;
 Matches 191; Conservative 0; Mismatches 206; Indels 0; Gaps 0;
 Qy 36 CAAGATGATCATGAGGGCCACCGGTGAACGGCCACTACTTCAAGTGCAGAGGGCGAGGGCGGA 95
 Db 106 CGACATCCACTTCACGGCTCCATCAACGGCCACGAGTTCGACATGTTGGGGGAGGAAA 165
 Qy 96 CGGCAACCCCTTTCGCGGCAACCCAGACATGAGNATCCAGTACCAGAGGGCGCCCCCT 155
 Db 166 AGGCGACCCGAAACGCGCGGCTCGTGTGTGACCAAGGAGGATCCACCAAGGGTCCCTGTAA 225
 Qy 156 GCCCTTCGCTTCGACATCTCGGCCCTCGTGTGAGTACGGCAGCAGGACCTTCGTGCA 215
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 Qy 216 CCACACGCGAGAGATCCCGGACTTCTTCAAGACAGAGGTTCCCGAGGGGTTCACTGGGA 275
 Db 286 CCGCGACGAGACCTTCGCGCTTTTCCAGGTCTCCATGTTGGAAGGATCGGGGTATGCAGTCTA 345
 Qy 276 GAGAACACACACTTACGAGGACGCGGCATCTTCAGCGCCACACAGACACACGACCTGGA 335
 Db 346 CCGCGTGTTCGACTTTGAGACGAGGACGAGCTGACTACCGAGTTTAAGTACTCTCTACGA 405
 Qy 336 GGGCAACTGCGTGTGATCTACAAGGTGAAGGTGCAAGGCAACCACTTCCCGCCGAGAGGCC 395

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Db 429 CTTACAGCCGCGACCAAGTCCGACGACGTGGAGATCCGCTGGCCAGCCACCAT 488
QY 387 CGACGCGCCCGGTGATGAAGAACAGAGCGGGCGGTGGGAGCCAGACCGAGGTGTGTA 446
Db 489 GATCCACGACTTCGCCATCACCAGAACTTGGTGTGTGGCCAGCACACGAGGTGTGTT 548
QY 447 CCCCAGAACGCGGTGTGTGGCGCGGAAAGTGTGATGCCCTGAAAGTGGCGCACCGGCA 506
Db 549 CAAAGTGCAGGAGATGCTGCGCGCGGGTCGCGCCGTGTGTGGACAGGAGAGAGCGTC 608
QY 507 CTTGATCTGCCACCACTACACAGCTACCGGAGCAAGAGCGCTGCGCGCCCTGACCAT 566
Db 609 GGGCTTGGGCTCTCCCGAAGCGCGCGGACCGCTCGGAGATGGCGTGGTGGACGT 668
QY 567 GCCCGGCTTCCACTTACCGCATCCGGCTCCAGATGTCGCGAAGAGAGAGAGCGAG 624
Db 669 GCCGGAAGTCTTCTGCTTCCACTGTGGAACGCGGTGGAGGACGAGGGCGGCGAG 726

RESULT 7
CF864358 700 bp mRNA linear EST 31-OCT-2003
LOCUS ps25009p17f USDA-IFAPS:Expression of Phytophthora sojae genes
DEFINITION during infection and propagation_s25 Phytophthora sojae cDNA clone
s25009p17 5, mRNA sequence.
ACCESSION CF864358
VERSION CF864358.1 GI:39118984
KEYWORDS EST...
SOURCE Phytophthora sojae
ORGANISM Phytophthora sojae
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
Phytophthora.
1 (bases 1 to 700)
Tyler,B.
Tyler,B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
VBI
1890 Pratt Dr., Blacksburg, VA 24061, USA
Tel: 540-231-7318
Email: bmtyle@vt.edu
PCR Primers
FORWARD: BK reverse primer
BACKWARD: BK reverse primer
Plate: 009 row: P column: 17
Seq primer: BK reverse primer
High quality sequence stop: 700.
Location/Qualifiers
1..700
/organism="Phytophthora sojae"
/mol_type="mRNA"
/db_xref="taxon:57593"
/clone="s25009p17"
/tissue_type="Zoospores"
/cell_lines="P6497"
/clone.lib="USDA-IFAPS:Expression of phytophthora sojae
genes during infection and propagation_s25"
/note="vector: pBK-CMV; Site_1: BcoRI; Site_2: XhoI"

ORIGIN
source
Query Match 9.7%; Score 66.4; DB 7; Length 700;
Best Local Similarity 45.7%; Pred. NO. 0.0014;
Matches 269; Conservative 0; Mismatches 316; Indels 3; Gaps 1;

QY 66 CCACCTACTTCAGTTCGAGGCGGAGGCGGACGGAACCCCTTCGCGGCGCACCGACAT 125
Db 103 CGCCACACACAGAGCCACACGCTGGATGGCATCAGCCCGCGCGCGACCTCCACCGT 162
QY 126 GAGATCCACGTGACCGGAGGCGCGCCCTCGCCCTTCGCTTCGACATCCTGGCCCGCTG 185
Db 163 GAG---CTCCGTCGCCACGCTCGCGCGCGGACGACAGATCGCCGCCACCGCGCGCG 219
```

```
QY 186 CTCGAGTAGCGGACGAGACCTTCGTGCACACACCGCGGAGATCCCGGACTTCTTCAA 245
Db 220 CTTCTCCACGGGTCAATGGCTGACGAGGTGTCTCCCAAGGAGCGCATCGACGTATCTA 279
QY 246 GCAGAGCTTCCCGAGGGTTTACCTTGGAGAGAACCCACCTACGAGGACGGCGGCAT 305
Db 280 CGACTACTCTCCATGAGCGCATCTCGAGTCCCGGCTCATCGGCGTCTGTGGCGCTCCGG 339
QY 306 CTTGACCGGCCACCGAGACACGACCTTGGAGGGCACTGCCTGATCTACAAGGTGAGGT 365
Db 340 CTTGCGAGGACTCAGCAACTTGGCTGTCCAAACGAGAGACCATCAAGTACGAGGACATCC 399
QY 366 GCACGCGACCAACTTCCCGCGGACCGGACCTGTATGAAGAAACAAGAGCGGGGTGGGA 425
Db 400 GCAGTTCCCGCGCTCCACCGTGGAGGCCACCGCGGAGAGCTCGTCTTGGCGACCTGA 459
QY 426 GCCACGACCGAGTGTGTATCCCGAGAACGGCGTGTGTGCGGCGGAAAGTGTATGCG 485
Db 460 GGGCTTCCGCGTGTGTGATCGCGCGCGCTTCCACTGTCTACGAGGGCTACGCCATGCG 519
QY 486 CTTGAAGGTGGGCGACCGGACCTGTATCTGCCACCACTACACGAGTACCGGAGCAAGAA 545
Db 520 CGAGACGGCGCTGCCCACTTGGCGTCACTGATACCTCTCGGCATCACTTCTGCTGTGAC 579
QY 546 GCGCGTGGCGCGCTTACCATGCGCGGCTTCCATTCACCGACATCCGCGCTCCAGATGCT 605
Db 580 CAAACGCGCGCGCGCTGAACCGGACTTCAACGTGGCGGCGCTCATGATCTGAACGA 639
QY 606 GCGGAAGAGAGAGGACGAGTACTTCGAGCTGTACGAGGCGGCGGCTGCGG 653
Db 640 CCACCTGAAGGTGCCCGGCGTGTGCGGTACGACCGCGCTCATCGGGCC 687
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```
RESULT 8
BZ422085 624 bp DNA linear GSS 10-DEC-2002
LOCUS id49d07.b1 WGS-Sbicolorf (DH5a methyl filtered) Sorghum bicolor
DEFINITION genomic clone id49d07 5', Genomic survey sequence.
ACCESSION BZ422085
VERSION BZ422085.1 GI:26370029
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 624)
Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,S., Muller,S., Nascimento,L.,
Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id49 row: d column: 07
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 624.
Location/Qualifiers
1..624
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="id49d07"
/lab_host="DH5a"
/clone.lib="WGS-Sbicolorf (DH5a methyl filtered)"
/note="Site_1: Xba I; Site_2: Xba I; The vector was
```

```
FEATURES
source
```

digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed into DH5a."

ORIGIN

```

Query Match      9.6%; Score 65.8; DB 8; Length 624;
Best Local Similarity 48.1%; Pred. No. 0.0018;
Matches 187; Conservative 0; Mismatches 202; Indels 0; Gaps 0;

QY 79 TCGAGGCGGAGGCGGACGGCAACCCCTTCGCCGGCACCCAGAGCATGAGAAATCCACGTG 138
DB 58 TTCCACGTACCGTGTGGGAGCCACGACGCTGGGATCCACCGGTGAGCATCGGGCG 117

QY 139 ACCGAGGCGGCCCTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 198
DB 118 CCGCGAGAGAGCCCAACACGAGCGGGGTGCACATCCAGGCTCTCTCCAACTGCGCGTC 177

QY 199 AGCAGGACCTTCGTGCACACACCGCGGAGATCCCGACTTCTTCAAGCAGAGCTTCCCC 258
DB 178 ACGGACTCGGCGGTGGCCACCGGAGCACTGCGTCTCCGTGGCCCGGGCGCTCCGAC 237

QY 259 GAGGCTTCACTCTGGGAGAGAACACACCTACGAGAGCGGCGCATCTTGACCGCCAC 318
DB 238 GTGGTGGTGTCCGGGTGTCTGGCGGCCCGCGGACGCGCATCAGCGTCCGCGCTCGGC 297

QY 319 CAGGACACAGCTCTGGGCGCACTGCTCTGATCTACAGGTGAAGGTGCACGCGCACCAAC 378
DB 298 AGGTACCCCGGCGAGAGAGAGCTCCCGCGGTGCGGTGGCCAACTGCACTCCCTCGCGGC 357

QY 379 TTCCCGCGCGAGCGGCCGCTGATGAGAAACAAGAGCGCGCGCTCGGAGCCCGACCGAG 438
DB 358 ACCTCCAAAGCGGTGCGCATCAAGACGTGGCGCGCGGCGCACCTGGCCCAACCGCGTCAAC 417

QY 439 GTGGTGTACCCGAGAACGGGTGTGTGTG 467
DB 418 GGCCTCGTCTTCGAGGACATCGTCATGAG 446

```

CC424389 982 bp DNA linear GSS 19-MAY-2003
 PUNHKS3TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBtra491I09,
 genomic survey sequence.

CC424389
 CC424389

VERSION
 CC424389.1 GI:30904479

KEYWORDS
 GSS.

SOURCE
 Zea mays

ORGANISM
 Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
 1 (bases 1 to 982)

AUTHORS
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Rennick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.

TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: PUNHKS3TD

Contact: Cathy Whitelaw

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..982

/organism="Zea mays"

FEATURES
 source

ORIGIN

```

Query Match      9.6%; Score 65.8; DB 8; Length 982;
Best Local Similarity 46.2%; Pred. No. 0.0018;
Matches 294; Conservative 0; Mismatches 337; Indels 6; Gaps 2;

QY 28 ATGCGCATCAAGATGATATCATGAGGCGCACCGGTGAGACGCCACTTCAAGTGGAGGGC 87
DB 263 AAGGGCGTCCAGTGGTGGCGACGCTCGTGTCAACCAACCGCTGGCGGACTACAAGGAC 322

QY 88 GAGGGCGGCGCAACCCCTTCGCCGGCACCCAGAGCATGAGATCCAGTGCACGAGGCG 147
DB 323 GCGCGGGCATCTACTTGGTCTTTCGAGGGCGGACGCCCGACAGCCGCTCGACTGGGSC 382

QY 148 GCGCCCTCTGCTTCCCTTTCGACATCTCTG---GCCCTCTGCTGCGAGTACGCGAGCAGG 204
DB 383 CCGGACATGATCTGCGAGCGACGACGAGTACTCCAACGGGCGGGCGCACCGGACACG 442

QY 205 ACCTTCGTGCACACACCGCGGAGATCCCGACTTCTTCAAGCAGAGCTTCCCGAGGGC 264
DB 443 GGGGCGGACTTTCGCCCGCGCGCGGACATGACCACTCAACCCCGCGGTGCGAGCAGAG 502

QY 265 TTCACTGGGAGAGAACCAACCTTACGAGGACGCGGCGCATCTTGACCGCCACCGAGGAC 324
DB 503 CTCTCGGACTGCTCAACTGGCTCAAGTCCGACCTCGGCTTCGAGCGGTGGCGCTCGAC 562

QY 325 ACAGCTGTGAGGGCAACTGCTCTGATCTCAAGGTGAAGGTGACGCGGACCACTTCCCC 384
DB 563 TTGCGCAAGGGGTACTTCCCGCGCGCTCGCCAAAGGTGTACGTGACAGCAGCCGCCACC 622

QY 385 GCGGAGCGCGCGTGTATGAAGAACAGAGCGCGCGCTGGAGCGCCAGCACCGAGGTGGT 444
DB 623 TTGCTGCTGCGCGAGATATGAGC---TCCCTCCACTACGACGCGCAACGCGGAGCGCTCC 679

QY 445 TACCCCGAGAACGCGGTGCTGTGCGCGCGGAAAGTGTGATGCGCCCTGAAGGTGGCGACCG 504
DB 680 AGCAACACGAGCGCGCGGACAGGAGGCTGTGTCAACTGGGCGGCGAGCGGTGGCGGCGCC 739

QY 505 CACCTGATCTGCCACCATACACAGCTACCGGAGCAAGAGGCGCTCGCGCCCTGACC 564
DB 740 GCGGCGGCTTCTGATTTACCAACAGGGGCTGTCTGAGGGGCGCTTCAGGGCGAGCTG 799

QY 565 ATGCCCGGCTTCCACTTCAACGACATCCCGGTTCAGATGCTGCGGAGAAAGAGAGCAG 624
DB 800 TGGCGCATGAAGGACGCGCAACCGCAAGGCGCGCGGATGATCGGTGCTGCGCGGAGAG 859

QY 625 TACTTCGAGCTGACGAGCGGCGAGCTGCGCCCGGTACA 661
DB 860 GCGGTACGTTCTGTCGACAAACACCGACACCGGCTCCA 896

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RESULT 10

CB651092/c

LOCUS

DEFINITION

clone OSJNB15018 3', mRNA sequence.

ACCESSION

CB651092

VERSION

CB651092.1

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

REFERENCE

1 (bases 1 to 794)

AUTHORS

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

CB651092 794 bp mRNA linear EST 08-APR-2003

OSJNB15018.r OSJNB Oryza sativa (japonica cultivar-group) cDNA

clone OSJNB15018 3', mRNA sequence.

ACCESSION

CB651092

VERSION

CB651092.1

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

REFERENCE

1 (bases 1 to 794)

AUTHORS

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

TITLE	Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
JOURNAL	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
COMMENT	Unpublished (2003) Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210089, Tucson, AZ 85721-0089, USA Tel: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu PCR Primers FORWARD: gta aaa cga cgg cca gtg BACKWARD: gga aac agc tat gac cat g Plate: 15 row: 0 column: 18 Seq primer: gga aac agc tat gac cat g. Location/Qualifiers 1..794
FEATURES	source

Mon Dec 13 08:35:06 2004

Db 431 GACAAGCAGAAGAACGCATCAAGGTGA 404

RESULT 12
CKI199961 821 bp mRNA linear EST 08-DEC-2003
LOCUS
DEFINITION FGAS008468 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
aestivum cDNA, mRNA sequence.

ACCESSION
CKI199961
CKI199961.1 GI:39562351

KEYWORDS
EST.

SOURCE
Triticum aestivum (bread wheat)

ORGANISM
Triticum aestivum

REFERENCE
1 (bases 1 to 821)

AUTHORS
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.

TITLE
Functional Genomics of Abiotic Stress in Wheat and Canola Crops

JOURNAL
Unpublished (2003)

COMMENT
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas.estseqs.usask.ca

This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [101,701].
Plate: L3C111 row: K column: 01.
Location/Qualifiers
1..821
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 3 Gate 6"
/note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
control, cold-acclimated and salt stressed wheat cultivar
Norstar. 7 mRNA populations were combined before
constructing the library; 7 day non-acclimated roots, 1,
23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
hours and 6 hours treated roots with 200mM NaCl.
Non-acclimated and cold-acclimated plants were grown in
vermiculite while salt stressed plant were grown
hydroponically. First strand synthesis in this library was
done in the presence of methylated dCTP thereby protecting
from internal cleavage with NotI."

FEATURES
source

ORIGIN
Query Match 9.4%; Score 64.6; DB 7; Length 821;
Best Local Similarity 48.1%; Pred. No. 0.0032;
Matches 215; Conservative 0; Mismatches 229; Indels 3; Gaps 1;

QY 104 CTTTCGCGGACCCAGAGCATGAGATCCAGCGGGGCGCCCTCGCCTTCG 163
Db 293 CCCCCGCGACAAACACCGCCCCCGCGCGCGACCTCTTCTCCCATCCCGG 352
QY 164 CTTTCGACATCTGCGCCCTCTCTCGAGTACGGCAGGAGACCTTCGTGACCAACCG 223
Db 353 CGCCCGGACAAACACGCGCGGGTTCGCGCGCGCAAGATGAACGGCAGCCTCAACGGGC 412
QY 224 CGGAGATCCCGACTTCTTCAGACGAGCTTCCCGAGGGTTCACCTGGGAGAGACCA 283
Db 413 CCGGCTCTATCGGGTCCGCGCAAGCTCGCTTCGGCGCCACCAACACAGCAG--GCCG 469
QY 284 CCACCTACGAGGACGGCGGCATCTCTGACCGGCCCAACAGACACAGCAGCTGGAGGGCACT 343

Db 470 ACCGTACAAACGTAGCTCGCCGCGCAAGCCTAGCGCAACGCCCAACG 529

QY 344 GCCTGATACAAAGGTGAAGGTGACGGCACCACCACTTCCCCCGCGAGCGGCCCGTATGA 403

Db 530 CCAACGGCATGTAGCGTCCCAAGCCCAACACCAACATGAACACGGGTTCGGGTCA 589

QY 404 AGAACAGAGCGGGCTGGCGAGCCAGCACCGAGGTGGTGTACCCCGAGAACCGCGTGC 463

Db 590 ACAAGATGGCTCCCGCGCGGGGTACGCGCACTTCAACAGCGGCAACGAGGGGTGA 649

QY 464 TGTGCGGCGGAACGTGATGCGCCCTGAAGTGGGCGACCGGCACCTGATCTGCCACACT 523

Db 650 AGAGCTACTTCAACAAAGTCCATCGCGAGCGCGCCAGCAACACAGCAGCGACCACT 709

QY 524 ACACCAAGTACCGGAGCAAGAGGCG 550

Db 710 TCAGCGCTACGCGCGCAAGAGGCG 736

RESULT 13
BI386976 613 bp mRNA linear EST 26-AUG-2003
LOCUS
DEFINITION BFL26 001679 Amphioxus 26hr cDNA library (Name convention: BFL26 or
MPMGp531) Branchiostoma floridae cDNA clone MPMGP531N0799 5', mRNA
sequence.

ACCESSION
BI386976
BI386976.1 GI:30921865

KEYWORDS
EST.

SOURCE
Branchiostoma floridae (Florida lancelet)

ORGANISM
Branchiostoma floridae

REFERENCE
1 (bases 1 to 613)

AUTHORS
Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J.,
Hewig, R., Vingron, M. and Lehrach, H.

TITLE
New evidence for genome-wide duplications at the origin of
vertebrates using an amphioxus gene set and completed animal
genomes

JOURNAL
Genome Res. 13 (6A), 1056-1066 (2003)

MEDLINE
22683279

PUBMED
12799346

COMMENT
Contact: Panopoulou G
Laboratory 145, Dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoul@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (<http://www.rzpd.de/>)
PCR Primers
FORWARD: 5' CCCCAGCTTACATTTATGCTTCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATTACCGCAGCTGGGAAAGGGGATGTG 3' (M13FSP)
Insert Length: 1 Std Error: 0.00
Seq primer: 5' CCGTCCGAATTCGGGT-3' pSport3/86
High quality sequence stop: 613.
Location/Qualifiers
1..613
/organism="Branchiostoma floridae"
/mol_type="mRNA"
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/clone="MPMGp531N0799"

FEATURES
source

/tissue_type="whole embryo"
 /dev stage="26 hrs (neurula stage)"
 /lab host="E.coli, XLI blue"
 /clone lib="Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMP531)"
 /note="Vector: pSport1 (Gibco BRL); Site 1: SalI, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTCTAGATCGGAGCGGCC (T)15-3' and a SalI 5'-TCGACCCAGCGTCCG-3' adapters (Gibco BRL)."

ORIGIN

Query Match 9.3%; Score 64.2; DB 4; Length 613;
 Best Local Similarity 47.6%; Pred. No. 0.0039;
 Matches 189; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 36 CAAGATGTACATGAGGACCGTGAACGGCACCTACTTCAAGTGCAGGGCGAGGCGGA 95
 DB 88 CGACATCCACCTTCAGGCTCCATCAAGGGCCAGGTTCCAGATGTGGGGGAGGAAA 147
 QY 96 CGGCAACCCCTTCGCGGACCCAGAGCATGAGATCCACGTGACCGAGGGCGCCCCCT 155
 DB 148 AGGCAACCCGAAACGCGCGCTGGTGCACACAGCGAAATCCACCAAGGGTGCCTGAA 207
 QY 156 GCGCTTCGCTTCGACATCTCGGCCCTGCTGGAGTACGCGACGAGGACCTTCGTGCA 215
 DB 208 GTTCTCTCCCTACTGATATCCCCACCTCGGTACGGGTACTACAGTACTTCCCTA 267
 QY 216 CCACACCCCGAGATCCCGCACTTTTCAACAGAGCTTCCCGAGGGCTTCACTGGGA 275
 DB 268 CCGGACGAGCCCTCGCTTCCAGGCTCCATGTTGAAGATCGGGGTATGAGCTA 327
 QY 276 GAGAACCAACCTACGAGGAGCGGCGATCTGATCCGCCACAGGACACGAGCTTGA 335
 DB 328 CCGGTGTTCGACTTGAAGACGAGGCAAGCTACTACCGAGTTTAAGTACTCTCTACA 387
 QY 336 GGGCAACTCGCTGATCTACAAGGTGAAGTGCAGGCGACCAACTTCCCGCGAGCGCC 395
 DB 388 GGGTTCCCATATCAAGCGGACATGAGCTATGGAAGCGTTTCCCTGATGAGCGCC 447
 QY 396 CGTGTGTAAGACAGAGCGCGGCTGGAGCCGAGC 432
 DB 448 AGTCATGACCAAGCCAGATTGTCGACCAAGGACGGCTGC 484

RESULT 14

BI386699

LOCUS

DEFINITION BFL26_001402 Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMP531) Branchiostoma floridae cDNA clone MPMP53111370 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

1 (bases 1 to 643)
 Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J., Herwig, R., Vingron, M. and Lehrach, H.
 New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal genomes
 Genome Res. 13 (6A), 1056-1066 (2003)
 22683279
 12799346
 Contact: Panopoulou G
 Laboratory 145, Dept. Lehrach
 Max-Planck-Institut fuer Molekulare Genetik
 Ihnestr. 63-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1235
 Fax: +49 30 8413 1128

Email: panopoul@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above EST is generated is available at the amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>
 Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (<http://www.rzpd.de>)

PCR Primers

FORWARD: 5' CCCAGCGTTTACACTTATGCTTCGGCTCG 3' (M13RSP)

BACKWARD: 5' GGTATTACCGAGCTGGGAAAGGGGATGTG 3' (M13FSP)

Insert Length: 1 Std Error: 0.00

Seq primer: 5'-CCGCTCGGAATTCGGGT-3', pSport3/86

High quality sequence stop: 643.

Location/Qualifiers

FEATURES

source

1..643
 /organism="Branchiostoma floridae"
 /mol_type="mRNA"
 /db_xref="taxon:7739"
 /clone="MPMP53111370"
 /tissue_type="whole embryo"
 /dev stage="26 hrs (neurula stage)"
 /lab_host="E.coli, XLI blue"
 /clone_lib="Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMP531)"
 /note="Vector: pSport1 (Gibco BRL); Site 1: SalI, KpnI, EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTCTAGATCGGAGCGGCC (T)15-3' and a SalI 5'-TCGACCCAGCGTCCG-3' adapters (Gibco BRL)."

ORIGIN

Query Match 9.3%; Score 64.2; DB 4; Length 643;
 Best Local Similarity 47.6%; Pred. No. 0.0039;
 Matches 189; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 36 CAAGATGTACATGAGGACCGTGAACGGCACCTACTTCAAGTGCAGGGCGAGGCGGA 95
 DB 77 CGACATCCACCTTCAGGCTCCATCAAGGGCCAGGTTCCAGATGTGGGGGAGGAAA 136
 QY 96 CGGCAACCCCTTCGCGGACCCAGAGCATGAGATCCACGTGACCGAGGCGCCCCCT 155
 DB 137 AGGCGACCGAAACGCGCGCTCGCTGGTACCAAGGATCCACCAAGGGTCCCTGAA 196
 QY 156 GCGCTTCGCTTCGACATCTCGGCCCTGCTGGAGTACGCGACGAGGACCTTCGTGCA 215
 DB 197 GTTCTCTCCCTACTGATATCCCCACCTCGGTACGGGTACTACAGTACTTCCCTA 256
 QY 216 CACACCGCGGAGATCCCGCACTTTTCAAGCAGAGCTTCCCGAGGGGTTCACTGGGA 275
 DB 257 CCGGACGAGACCTCGCTTTCCAGGCTCCATGTTGAAGATCGGGGTATGAGTCTA 316
 QY 276 GAGAACCAACCTACGAGGAGCGGCGATCTGACCGGCCACAGGACACGAGCTGGA 335
 DB 317 CCGGTGTTCGACTTGAAGACGAGGAGGAGTACTACTCCGAGTTAAGTACTCTACA 376
 QY 336 GGGCAACTCGCTGATCTACAAGGTGAAGTGCAGGACCAACTTCCCGCGAGCGCC 395
 DB 377 GGGTTCCCATATCAAGGGCGGACATGAAGCTGATGGGAAGCGGTTTCCCTGAGCGGCC 436
 QY 396 CGTGTGTAAGAACAGAGCGCGGCTGGAGCCGAGC 432
 DB 437 AGTCATGACCAAGCCAGATTGTCGACCAAGGACGGCTGC 473

RESULT 15

CNS02EOD/c

LOCUS

CNS02EOD 681 bp DNA linear GSS 01-SEP-2000

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 262H14 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL193990

VERSION AL193990.1 GI:7832096

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Telsostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE 1
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

REFERENCE 2
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)

REFERENCE 3 (bases 1 to 681)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES
source
1..681
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="262H14"
/clone_lib="G"
/note="Genoscope sequence ID : C0AG262DD07LP1-end : T7"

ORIGIN
Query Match 9.3%; Score 64; DB 9; Length 681;
Best Local Similarity 41.9%; Pred No. 0.0043;
Matches 176; Conservative 27; Mismatches 217; Indels 0; Gaps 0;

QY 18 GAAGGAGAGTATGCGCATCAAGATGATCATGGAGGGACCGTGAACGGCCACTACTTCAA 77
DB 433 CGAGACRATTTTWTATATATTTGTCDACRACAAWACAAACAAACAAACAAACAACTA 374

QY 78 GTGCGAGGGCGGGCGGCGGCAACCCCTTCGCGGACCCAGAGCATGAGATCCACGT 137
DB 373 CAACAAAWACAAACAGGGGGGCAACAAACAGACACGACGACACACAAACAAACACRA 314

QY 138 GACCGAGGGCGCCGCCCTTCGCTTCGACATCTCGCTTCGCTTCGCTTCGCTTCGCTTCG 197
DB 313 CGGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 254

QY 198 GAGCGAGGACCTTCGTGACACACGCGGAGATCCCGACTTCTTCAGCAGAGCTTCCC 257
DB 253 CAACRACGCGGCGGACRACAAACAAACAAACAAACAAACAAACAAACAAACAAACNA 194

QY 258 CGAGGGCTTCACCTGGGAGAGAACCAACACCTACGAGACGGCGGCGATCTCTGACCGCCA 317
DB 193 CGGACAA 134

QY 318 CCAGGACACACGCTGGAGGGCACTGCTGATCTTACAAAGTGAAGGTGCAACGGCACCAA 377
DB 133 CAACAAACAA 74
QY 378 CTTCCCGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 437
DB 73 AAACACACACACGCGGCAACAAACAAACAAACAAACAAACAAACAAACAAACRA 14

Search completed: December 10, 2004, 18:44:40
Job time : 3731 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2004, 16:17:09 ; Search time 100 Seconds
(without alignments)
4893.120 Million cell updates/sec

Title: US-09-976-673-11
Perfect score: 687
Sequence: 1 atggtgagcgctgtgaa.....tgcccgagagggccaactga 687

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297.4	43.3	723	4	US-10-152-296-1
2	253.4	36.9	1482	4	US-09-977-897-1
3	253.2	36.9	720	4	US-09-839-850-1
4	176.6	25.7	678	3	US-09-459-956-6
5	153.8	22.4	801	3	US-09-459-956-7
6	145.4	21.2	699	3	US-09-459-956-5
7	121.6	17.7	1104	3	US-09-277-716-30
8	121.6	17.7	1104	4	US-09-609-161B-30
9	121.6	17.7	1279	3	US-09-277-716-31
10	121.6	17.7	1279	4	US-09-609-161B-31
11	110.6	16.1	720	3	US-09-172-063-14
12	110.6	16.1	720	4	US-09-316-919-15
13	110.6	16.1	720	4	US-09-602-641-14
14	110.6	16.1	720	4	US-09-316-920A-15
15	109.8	16.0	690	3	US-09-459-956-2
16	109	15.9	717	4	US-09-513-783A-43
17	109	15.9	717	4	US-09-430-656-43
18	109	15.9	720	3	US-08-911-825-3
19	109	15.9	720	3	US-08-974-737-3
20	109	15.9	720	3	US-08-706-408-3
21	109	15.9	720	3	US-09-094-359-9
22	109	15.9	720	3	US-09-172-063-12
23	109	15.9	720	3	US-09-172-063-17
24	109	15.9	720	4	US-09-465-142-3
25	109	15.9	720	4	US-09-316-919-13
26	109	15.9	720	4	US-09-316-919-18
27	109	15.9	720	4	US-09-575-847-3

28	109	15.9	720	4	US-09-602-641-12	Sequence 12, Appl
29	109	15.9	720	4	US-09-602-641-17	Sequence 17, Appl
30	109	15.9	720	4	US-09-704-463-9	Sequence 9, Appl
31	109	15.9	720	4	US-09-316-920A-13	Sequence 13, Appl
32	103	15.9	720	4	US-09-316-920A-18	Sequence 18, Appl
33	109	15.9	720	4	US-10-071-976-3	Sequence 3, Appl
34	109	15.9	768	3	US-09-172-063-28	Sequence 28, Appl
35	109	15.9	768	3	US-09-172-063-33	Sequence 33, Appl
36	109	15.9	768	4	US-09-602-641-28	Sequence 28, Appl
37	109	15.9	768	4	US-09-602-641-33	Sequence 33, Appl
38	109	15.9	972	3	US-09-172-063-30	Sequence 30, Appl
39	109	15.9	972	4	US-09-602-641-30	Sequence 30, Appl
40	109	15.9	1623	4	US-09-513-783A-33	Sequence 33, Appl
41	109	15.9	1623	4	US-09-430-656-33	Sequence 33, Appl
42	109	15.9	2439	4	US-09-513-783A-3	Sequence 3, Appl
43	109	15.9	2439	4	US-09-513-783A-5	Sequence 5, Appl
44	109	15.9	2439	4	US-09-430-656-3	Sequence 3, Appl
45	109	15.9	2439	4	US-09-430-656-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-152-296-1
; Sequence 1, Application US/10152296
; Patent No. 6723537
; GENERAL INFORMATION:
; APPLICANT: Peelle, Beau
; TITLE OF INVENTION: Directed Evolution of Protein in Mammalian Cells
; FILE REFERENCE: 021044-000110US
; CURRENT APPLICATION NUMBER: US/10/152,296
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/291,871
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mammalian
; OTHER INFORMATION: codon-optimized variant (DsRED) of Discosoma sp.
; OTHER INFORMATION: "red" red fluorescent protein (RFP)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
; OTHER INFORMATION: DsRED
US-10-152-296-1

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Db	21	CGTCATCAAGGAGTTTCATGCGCTTCAAGTGGCATGGAGGCGCACCGTGAACGGCCACGA	80				
QY	72	CTTCAAGTGGAGGCGGAGGCGGAGCGGCAACCCCTTCCCGGCGCACCCAGAGCATGGAAT	131				
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QY	132	CCACGTGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	191				
Db	141	GAAGGTGACCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	200				
QY	192	GTACGGGAGAGGACCTTCGTGTCACCAACCGCGGAGATCCCGGACTTCTTCAAGACAG	251				
Db	201	GTACGGCTCCAGGTGTACGTGAAGCACCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	260				
QY	252	CTTCCCGGCGGCTTCACTCGGTGGAGAGAACCAACCACTTACGAGGAGCGGCGGCGGCGG	311				

Db 261 CTTCCCGAGGGCTTCAAGTGGGAGCGCGTATGAATCTCGAGACGGCGCGTGTGAC 320
QY 312 CGCCCAACAGGACACACCGCTTGGAGGCAACTGCTGATCTACAAGGTGAAGTGCACGG 371
Db 321 CGTGACCCAGGACTCTCCCTTGCAGGACGGCTGCTTCTATCTACAAGGTGAAGTTCATCGG 380
QY 372 CACCAATCTCCCGCAGCGCCCGCTGATGAAGAACAGAGCGGCGCTTGGAGGCCAG 431
Db 381 CGTGAACCTCCCTCCGACCGCCCGCTAATGCAAGAGACCATGGCTTGGAGGCCCTC 440
QY 432 CACGAGGTGTGTACCCCGAGAGACGGCGTCTGTGCGCGCGAAACGCTGATGCGCCCTGAA 491
Db 441 CACGAGCGCTGTACCCCGCAGCGCGTGTCTGAAGGCGAGATCCACAAGGCCCTGAA 500
QY 492 GGTGGGCGACCGGCACTGTATCTCCACCACTACACAGCTACCGGAGCAAGAGGCCGT 551
Db 501 GCTGAAGGACGCGCGCC-----ACTACCTGTGTGAGTTCAAGAGTATCTACATGGCCAA 554
QY 552 GCGCGCTGACCATGCCCGCTTCCACTTCAACCGACATCCGGCTCCAGATGCTGCGAA 611
Db 555 GAAGCCCGTGCAGTGTCCCGCTACTACTAGTGCATCTCAAGCTGCACATCACTCCCA 614
QY 612 GAAGAGGACGAGTACTTC---GAGCTGTACGAGCGCAGCGTGGCCGCTACAGGACCT 668
Db 615 CAACGAGGACTACACCATCTGTGGAGCAGTACGAGCGACCGAGGCGCGCCACCACCTGTT 674
QY 669 CCCCAGAGGCC 681
Db 675 CTGGAGGAGGCC 687

RESULT 2

US-09-977-897-1

; Sequence 1, Application US/09977897

; Patent No. 6780974

; GENERAL INFORMATION:

; APPLICANT: Chen, Yih-Tai

; APPLICANT: Cao, Longquan

; TITLE OF INVENTION: A synthetic DNA encoding an orange seapen-derived green fluorescent

; FILE REFERENCE: 41856-5

; CURRENT APPLICATION NUMBER: US/09/977,897

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1482

; TYPE: DNA

; ORGANISM: *Perilousarcus gurneyi*

US-09-977-897-1

Query Match 36.9%; Score 253.4; DB 4; Length 1482;
Best Local Similarity 63.1%; Pred. No. 1.2e-43;
Matches 427; Conservative 0; Mismatches 241; Indels 9; Gaps 2;

QY 2 TGGTGGCGGCTGCTGAAGGAGTATCGCATCAGATGATGAGGCGCACCGTGA 61
Db 32 TGAAGAACAACCGGCTGAAGGAGATCATGAGCGCCCAAGGCCAGCGTGGAGGGCATCTGTA 91
QY 62 AGCGGCACCTACTTCAAGTGGAGGCGGAGGCGAGCGCAACCCCTTGCAGGCGCACCCAGA 121
Db 92 ACAACACCGTGTTCAGCATGGAGGCTTCGCAAGGGCAACGCTGTTCGGCAACACAGC 151
QY 122 GCATGAGATTCACGTGACGAGGCGCGCCCTTGCCTTGCATCTGAGATCTGCGCC 181
Db 152 TGATGAGATTCGGGTGACCAAGGCGCGCCCTTGCCTTGCATCTGAGCA 211
QY 182 CTGCTGCGAGTACCGGACGAGGACTTCGTGACCAACACCGCGGAGATCCCGGACTTCT 241
Db 212 TCGCTTCCAGTACCGGACCGGACTTCACCAAGTATCCCGACGACATCGCGACTACT 271
QY 242 TCAAGGAGAGCTTCCCGAGGGCTTCACTCTGGGAGAGAACCAACCATCTACGAGAGCGG 301

Db 272 TCGTGCAGAGCTTCCCTGCCGGCTTCTTACGAGCGGAACCTCGGCTTCGAGAGCGCG 331
QY 302 GCATCCTGACCGCCACAGGACACAGCTTGGAGGCACTGCTGATCTACAGGTGA 361
Db 332 CCATCGTGGACATCCGGAGCGACATCAGCTTGGAGGACGACAAAGTTCACCTACAGGTGG 391
QY 362 AGGTGCAGCGCACCAACTTCCCGCGAGCGCCCGCTGATGAAGAACAAAGAGCGCGGCT 421
Db 392 AGTACCGCGGCAACCGCTTCCCTAGCAACGCGCTGTGATGCAAGAGGCCATCTCGGCA 451
QY 422 GGGAGCCAGACCGAGGTGTGTACCCCGAGAGAGCGGCTGC---TGTGGCGCGGAGC 478
Db 452 TGGAGCCAGCTTCCAGGTGTGTATCATGAACAGCGCGCTGCTGTGGGCGAGGTGAGCC 511
QY 479 TGATCGCCCTGAAGGTGGCGGACCGGCACTGATCTGCCACCACTACACAGCTACCGGA 538
Db 512 TGGTGTACAAGCTGGAGAGCGGCACTACTACAGTGCACATGAAGACCTTCTACCGGA 571
QY 539 GCAAGAAGCGCGTGGCGCCCTGACCATGCGCGGCTTCCACTTCAACGACATCCGCGTCC 598
Db 572 GCAAGGCGCGGTG-----AAGGAGTTCCTGAGTACCTATTTCATCCACCGCGGTGG 625
QY 599 AGATCCTCGGAGAGAGAGGAGGAGTACTTTCGAGCTGACGAGCGGCGTGGCGCGGT 658
Db 626 AGAAGAACTACGTGGAGGAGGCGAGCTTCTGTGAGAGACGAGACCGCCATCGCCNAGC 685
QY 659 ACAGCGACCTGCCCCGAG 675
Db 686 TGACCACCATCGGCAAG 702

RESULT 3

US-09-839-650-1

; Sequence 1, Application US/09839650

; Patent No. 6645761

; GENERAL INFORMATION:

; APPLICANT: Stratagene

; TITLE OF INVENTION: Humanized Polynucleotide Sequence Encoding Renilla Mulleri Green

; Patent No. 6645761

; FILE OF INVENTION: Fluorescent Protein

; FILE REFERENCE: 25436/1755

; CURRENT APPLICATION NUMBER: US/09/839,650

; CURRENT FILING DATE: 2001-04-19

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 720

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Humanized R. mulleri polynucleotide

; NAME/KEY: misc.feature

; LOCATION: (1)..(720)

; OTHER INFORMATION: Humanized DNA sequence

US-09-839-650-1

Query Match 36.9%; Score 253.2; DB 4; Length 720;
Best Local Similarity 62.0%; Pred. No. 1.2e-43;
Matches 418; Conservative 0; Mismatches 253; Indels 3; Gaps 1;

QY 2 TGGTGGCGGCTGCTGAAGGAGTATCGCATCAAGATGTATATGAGGCGCACCGTGA 61
Db 20 TGAAGAACAACCTGCTGCGAGGAGTATGAGCTACAAGGTGAACCTGGAGGCGCATCTGTA 79
QY 62 AGCGGCACCTACTTCAAGTGGAGGCGGAGGCGAGCAACCCCTTGCAGGCGCACCCAGA 121
Db 80 ACAACACCGTGTTCACCATGGAGGCTGCGGCAAGGCAACATCTGTTCGCGACACGAC 139
QY 122 GCATGAGAAATCCACGTGACCGGCGCGCCCTTGCCTTGCCTTCGACATCTCGGCC 181
Db 140 TGGTGCAGATCCGCGTGACCAAGGCGCGCCCTTGCCTTGCCTTGCACATCTGAGCC 199

QY 182 CTTGCTCGAGTACGGCAGCAGACCTTCTGTCACACACCGCGGAGATCCCGACTTCT 241
Db 200 CCGCTTTCCAGTACGGCAACCGACCTTTACCAAGTACCCCAACGACATCAGGCACTACT 259
QY 242 TCAAGCAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACCAACCACTACGAGGACGGCG 301
Db 260 TCATCCAGAGCTTCCCGCGGGCTTCATGTACGAGCGCACCTCGCGCTACGAGGACGGCG 319
QY 302 GCATCTCTCGCGCCACCAAGACACAGACACAGCTGAGGCACTGCTGATCAACAGGTGA 361
Db 320 GCCTGGTGGAGATCCGAGGACATCAACCTGATTCGAGGACAAGTTCGTGTACCGCGTGG 379
QY 362 AGTGTCAAGCAGCAAACTTCCCGCGGACCGCGCTGATGAAGAAACAAAGAGCGGGCGGT 421
Db 380 AGTACAGGCGAGCAACTTCCCGAGCAAGCGCGCGCTGATGCAAGAACCATCTGGGCA 439
QY 422 GGGAGCCAGCAGCAGAGGTGTATCCCGAGAGAACCGCGTCTGTGGGCGCGGAAAGTGA 481
Db 440 TCGAGCCAGCTTCGAGGCGCATGATGATGAACAAACCGCGCTGCTGTGGGCGAGGTGATCC 499
QY 482 TGGCCCTGAAGGTGGGCGACCGGACCTGATCTGCCACCACTACACGAGCTACCGGAGCA 541
Db 500 TGGTGTACAGCTGAAACAGCGGCAAGTACTACAGCTGCCACATGAAGACCTGATGAAGA 559
QY 542 AGAAGCGGTGCGCGCTGACCAATGCCGGCTTCCACTTCACCGACATCCGGCTCCAGA 601
Db 560 GCAAGGCGGTG--GTGAAGAGTTCCTCCCTTACCACTTCATCCAGCAACCGCTCGAGA 616
QY 602 TGCTGCGGAAGAAGAGCAGAGTACTTCGAGCTGTACGAGGCGAGCGTGGCGGTGACA 661
Db 617 AGACCTAGTGGAGAGCGGGCTTCTGTGAGCAGCAGAGACCGGCATCGCCCAAGATGA 676
QY 662 GCGACCTGCCCGAG 675
Db 677 CCAGCATCGGCAAG 690

RESULT 4

US-09-459-956-6
; Sequence 6, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp
US-09-459-956-6

Query Match 25.7%; Score 176.6; DB 3; Length 678;
Best Local Similarity 60.2%; Pred. No. 6.9e-28;
Matches 293; Conservative 0; Mismatches 194; Indels 0; Gaps 0;

QY 17 TGAAGGAGATGATCGCATCAAGATGTACATGGAGGCGACCGTGAACGGCCACTACTTCA 76
Db 23 TCAAGGAGTTCATGAGGTTTAAGGTTGCGATGGAAGAAACGGTCAATGGGCAAGTTG 82
QY 77 AGTGGAGGGGAGGGGACGGCAACCCCTTCGCGGACCCAGAGCATGATCAACG 136

Db 83 AATAAGAGCGAAGAGAGGAGGCGCCATACGAAGGCCACAATACCGTAAAGCTTAAGG 142
QY 137 TCACCGAGGGCGCCCCCTTGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACG 196
Db 143 TAACCAAGGGGGAGCTTTGCCATTTGCTTGGGATAATTTGTACCAACAATTTCAATG 202
QY 197 GCAGCAGGACCTTCGTGCAACCAACCGCGGAGATCCCGACTTCTTCAAGCAGAGCTTCC 256
Db 203 GAAGCAAGGTATATGTCAAGCACCTCGCGACATACAGACTATAAAGAGCTGTCATT 262
QY 257 CCGAGGCTTCACTCTGGGAGAGAACCACTCTAGGAGCGGGGATCTTACCAGGCC 316
Db 263 CTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTGAAGACGGTGGCGTCTTACTG 322
QY 317 ACCAGCACACAGCGCTGAGGCGCACTGCCTGATCTACAAGTGAAGTGCACGCGACCA 376
Db 323 CCAGATTCAGTTTGCAGGATGCTGTTCACTACAAGTCAAGTTCATTGGCGTGA 382
QY 377 ACTTCCCGCGACCGCCCCGTGATGAAGAAACAGAGCGGGCTGGAGGCCAGCACCG 436
Db 383 ACTTTCTTCCGATGAGCTGTTATGCAAAAGAGACAATGGGCTGGGAAGCCAGCACTG 442
QY 437 AGTGGTGTACCCCGAGAACGCGCTGTCGCGCGGAAACGTGATGCGCTGAAGGTGG 496
Db 443 AGCTTTGTATCTCTCGTATGCGGTGTTGAAGAGAGAGATTCAATAGGCTCTGAAGCTGA 502
QY 497 GCGACCG 503
Db 503 AAGACGG 509

RESULT 5

US-09-459-956-7
; Sequence 7, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Clavularia sp
US-09-459-956-7

Query Match 22.4%; Score 153.8; DB 3; Length 801;
Best Local Similarity 58.4%; Pred. No. 3.5e-23;
Matches 289; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 10 GGCCTGCTGAAGGAGAGATATGCGCATCAAGATGTACATGGAGGCGACCGTGAACGGCCAC 69
Db 130 GGTGTGATTTAAACCAACAGACATGAAGATTAAAGCTGAAGATGAAGAAATGTTAAACGGCAT 189
QY 70 TACTTCAAGTGCAGGGCGGCGGCGACCGCAACCCCTTCGCGGCGCACCGAGCATGAGA 129
Db 190 GTTTTGTGATCGAAGGAGAGAGAAAGAAACCTTACGATGGGACACACACTTTAAAC 249
QY 130 ATCCAGCTGACCGAGGCGGCCCTTCGCTTCGATCTCGACATCTCTGCCCCCTGCTGC 189
Db 250 CTGAAGTGAAGAGAGGTGCGCTCTGCTTTTCTTACGATATCTTGTCAAACGCGTTC 309

190	Qy	GAGTACGGCAGCAGACCTTCGTGCACACACCCCGAGATCCCAGACTTCCTTCAAGCAG	249
310	Db	CAGTACGGAAACAGAGCATTCACAAATACCCAGACGATATAGCAGACTATTTCAAGCAG	369
250	Qy	AGCTTCCCCAGGGCTTCACCTGGGAGAGAACACCACTACAGAGCAGCGGCATCTCTG	309
370	Db	TGCTTCCGAGGGATATCTCGGAAAGAACCATGACTTTGNAGCAAGGCATGTCTC	429
310	Qy	ACGCCCAACAGCACCAGAGCCTGGAGGGCAACTGCCTGATCTCAAGGTGAAGGTGCAC	369
430	Db	AAAGTGAAAGTGACATAGCATGATGAGGAAGACTCCTTTATCTATGAAATTCGTTTGTAT	489
370	Qy	GGCACCACATCTCCCGCGCAGCGGCCGCTGATGAAGAACAGAGCGCGCTCGGAGCCC	429
490	Db	GGGATGAATTTCTCTCCCATATGGTCCGGTTATGAGAAATAAACTTTGAAGTGGGAACCA	549
430	Qy	AGCACCGAGGTGGTGTATCCCCGAGAACGGCGTGTGTCGG	470
550	Db	TCCACTGAGATTATGATCGTGGTGATGGAAGTGTGGTCTCG	590

RESULT 6

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US-09-459-956-5
; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEN
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1230-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Discosoma striata
US-09-459-956-5

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Query Match	21.2%	Score 145.4;	DB 3;	Length 699;
Best Local Similarity	56.3%;	Pred. No. 1.8e-21;		
Matches 272;	Conservative 0;	Mismatches 211;	Indels 0;	Gaps 0;
QY	14	TCGTCGAAGGAGATGCGCATCAAGATGTACATGTGGAGGGCCACCGTGAACGCCACTACT	73	
Db	20	TGATCAAGGAAGAATGTTGATCGATCTTCATCTGGAAGACGTTCAATGGGCACTACT	79	
QY	74	TCAAGTCGAGGGCGAGGGGAGCGCAACCCCTTCGCGCGCACCCAGAGCATGAGAAATCC	133	
Db	80	TTGAATAAAGGCAAAAGGAAAGACAGCGCTAATGAAGGCCAATAACGTCACGCTCG	139	
QY	134	AGGTGACACGAGGGCGCCCTCGCTCCCTTCGACATCTCGGCCCCCTGTCGCGAGT	193	
Db	140	AGGTTACACAGGTGTGACCTCTGCCATTGCTGGTCATATTTTGTGCCCAAAATTCAGT	199	
QY	194	ACGGCAGCAGGACCTTCGTGCACACACCGCCGAGATCCCGGACTTCTTCAAGCAGAGCT	253	
Db	200	ATGGAAGCAAGCATTTGTCCACCAACCATACATGATTATCTAAAGCTGTTCAT	259	
QY	254	TCCCGAGGGCTTCACCTGGGAGAGACCAACCACTTACGAGGACGGCGCATCTTCGACCG	313	
Db	260	TTCCGGAGGGATATACATGGGAACGGTTCATGCACTTTGAAGACGGTGGCTTGTGTTGTA	319	
QY	314	CCCACGAGACACCAAGCCTTGGAGGGCAACTGCCTGATCTTCAAGGTGAAGGTGCACGGCA	373	

```

320  TCACCATGATATCAGTTTGTGACAGCAACTGTTTCTACTACGACATCAAGTTCACTGGCT 379
374  CCAACTTCCCGCGACCGCCCTGTGTAGTGAAGAACAGACGCGCGCTGGGAGCCCGACGA 433
380  TGAACCTTTCTCCAAATGGACCCCTTGTGCAGAGAAGAACAACCTGGCTGGGAACCGACGA 439
434  CCGAGGTGGTGTAACCCCGAGACCGCGTGTGTGCGCCCGGAACGTGATGGCCCTGAAGG 493
440  CTGAGCGTTTGTATCCTCGTGATGTGTGTTGATAGGAGACATCCATCATGCTCTGACAG 499
494  TGG 496
500 TTG 502

RESULT 7
US-09-277-716-30
; Sequence 30, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROMUE, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING
; CURRENT APPLICATION NUMBER: US/09/277,716A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Pilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Pilosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-277-716-30

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Query Match	17.7%;	Score 121.6;	DB 3;	Length 1104;
Best Local Similarity	54.2%;	Pred. No. 1.5e-16;		
Matches	247;	Conservative	0;	Mismatches 209; Indels 0; Gaps 0
Qy	16	CTGAGGAGAGTATCGCATCAAGATGTACATGAGGGCACCGTGAAGCGGCACACTACTTC	75	
Db	64	CTGAAGAAGATTATGTCGGCAAAAGCTAGCGTTGAAGAAATCGTGAAACAATCACGTTTTT	123	
Qy	76	AAGTCGAGGGGAGGGGACGGCAACCCCTTCGCGGGACCCAGAGCATGAGAATCCAC	135	
Db	124	TCCATGGAGAGNTTTGGAAAGGCAATGTATTATTGGAAACCAATTGATGCAATCCGG	183	
Qy	136	GTGACCGAGGGGGCCCCCTTCGCTTCGCAATCGTGCGCCCTTCGTGCGAGTAC	195	
Db	184	GTTACAAAGGAGGTTCGCTTCCCATTCGCTTCGATATTGTTCCATAGCTTTCCAATAC	243	
Qy	196	GGCAGCAGGACCTTCGTGCACACACCGCGAGATCCCGACTTCTTCAAGCAGAGCTTC	255	
Db	244	GGGAATCGCACTTTACAGAAATACCCAGACGCAATTGCGGACTACTTTGTTCAATCATTC	303	
Qy	256	CCGAGGGCTTCACCTGGGAGAGAAACCAACCATCTACGAGACGGCGGCATCTGACCGCC	315	
Db	304	CGGCTGGAATTTTCTACGAAAGAAATCTAGGCTTTGAAGATGGCGCCATTTGTGCATT	363	
Qy	316	CACCAAGGACACGAGCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGGTGCACGGCAC	375	
Db	364	CGTTCAGATAAGTTTAGAGATGATAAGTTCCACTACAAAGTCGAGTATAGAGCAAC	423	

[illegible]

RESULT 8
 US-09-609-161B-30
 ; Sequence 30, Application US/09609161B
 ; Patent No. 6436682
 ; GENERAL INFORMATION:
 ; APPLICANT: Bryan, Bruce
 ; APPLICANT: Stent-Gorygi, Christopher
 ; APPLICANT: PROLUME, LTD.
 ; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
 ; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
 ; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
 ; FILE REFERENCE: 24729-121B
 ; CURRENT APPLICATION NUMBER: US/09/609,161B
 ; CURRENT FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: 09/277,716
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 60/102,939
 ; PRIOR FILING DATE: 1998-10-01
 ; PRIOR APPLICATION NUMBER: 60/089,367
 ; PRIOR FILING DATE: 1998-06-15
 ; PRIOR APPLICATION NUMBER: 60/079,624
 ; PRIOR FILING DATE: 1998-03-27
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 30
 ; LENGTH: 1104
 ; TYPE: DNA
 ; ORGANISM: Ptilosarcus gurneyi
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (34)..(747)
 ; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert A)
 US-09-609-161B-30

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Db      424  GGTTCCTCTAGTAACGACCGTGTATGCAAAAAGCCATCTCTGGCATGGAGCCATCGTTT 483
Qy      436  GAGTGTGTGTACCCCGAGAACGGCGTGTCTGTGCGGC 471
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Db      484  GAGTGTGTCTACATGAACAGCGCGTCTGTGCGGC 519
          |||||

RESULT 9
US-09-277-716-31
; Sequence 31, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A
; CURRENT FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; FEATURE:
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert B)
US-09-277-716-31

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RESULT 10
US-09-609-161B-31
; Sequence 31, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: *Ptilosarcus gurneyi*
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: *Ptilosarcus Green Fluorescent Protein (GFP) (insert B)*
US-09-609-161B-31

Query Match 17.7%; Score 121.6; DB 4; Length 1279;
Best Local Similarity 54.2%; Pred. No. 1.6e-16;
Matches 247; Conservative 0; Mismatches 209; Indels 0; Gaps 0;
QY 16 CTGAAGAGAGATATGCGCATCAAGATGACATGAGGAGGACCGGTGAACGGCCACTACTTC 75
Db 37 CTGAAGAGAGATATGCGGCAAAAGTAGCTTGAAGAAATCGTGAACAATCAAGTTT 96
QY 76 AAGTCCGAGGCGGAGGCGGCAACCCCTTCGCCGCGCACCCAGAGCATGAGATCCAC 135
Db 97 TCCATGGAAGGATTTGGAAAGGCAATGATATTTGGAACCAATGATGCAATCCGG 156
QY 136 GTGACGAGGCGGCGCCCTGCTGCTTGCCTTGCATCTGCGCCCTGCTGCGAGTAC 195
Db 157 GTTCAAAAGGAGGTCGCTTCCATTCGCTTTCGACATTTGTTCCATAGCTTTCCATAC 216
QY 196 GGCAGCAGACCTTGTGTCACACACCGCCGAGATCCCGACTTCTTCAAGCAGAGTTC 255
Db 217 GGGATTCGCACTTTCAAGAAATACCCAGACATTCGGGACTACTTTGTTCAATCAAT 276
QY 256 CCGGAGGCGCTTCACTCGGAGAGAACCAACCTACAGAGCGGCGGCTCCTGACCGCC 315
Db 277 CGGCTGGATTTTCTACGAAGAATCTACGCTTTGAAGATGCGGCAATTTGTGACAT 336
QY 316 CACAGGACACAGCCTGGAGGCAACCTGCTGATCTTCAAGGTGAAGGTGACCGGACC 375
Db 337 CGTTTCAGATATAGTTTGAAGATGATAAGTTCCACTACAAAGTGGAGTATAGAGGCAAC 396
QY 376 AACTTCCCGCGGAGCGGCGCTGATGAAGAACAGAGCGGCGCTGCGGAGCCGAGCAC 435
Db 397 GGTTCCTTAGTACGACCGCTGATGCAAAAGCAACCCATCTCGCATGAGGCAATCGTT 456
QY 436 GAGTGTGTATCCCGAGAAACGGGTGTGTGCGGC 471
Db 457 GAGGTGTGTCTACATGAACAGCGGCGTCTCTGTGTCG 492

RESULT 11

US-09-172-063-14
; Sequence 14, Application US/09172063
; Patent No. 6150176
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Llopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: MEASURING THE PH OF A BIOLOGICAL SAMPLE
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/172,063
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 09/094,359
; EARLIER FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 720
; TYPE: DNA
; ORGANISM: *Aequorea victoria*
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: EYFP-V68L/Q69K
US-09-172-063-14

Query Match 16.1%; Score 110.6; DB 3; Length 720;
Best Local Similarity 55.2%; Pred. No. 2.7e-14;
Matches 262; Conservative 0; Mismatches 204; Indels 9; Gaps 2;
QY 13 CTGCTGAAGGAGATATGCGCATCAAGATGTATATGAGGAGGACCGTGAAGCGCACTAC 72
Db 22 CTGTTACCGGGGTGCTGCTCCATCTCTGTGCGAGCTGGACGCGACGTAACGCGGCACAG 81
QY 73 TTCAAGTGGAGGCGGAGGCGGACGCAACCCCTTCGCCGCGCACCCAGAGCATGAGATC 132
Db 82 TTCAGCGTGTGCGGAGGCGGAGGCGATGCGCACTACGCAAGCTGACCTGAGTTC 141
QY 133 CACGTGACGAGGCGGCGCCCTTCCTTCGCTTCGACATCTCTGGCCCTCTGTGCGAG 192
Db 142 ATCTGCACAC---CGGCAAGCTGCGCTGCGCCACCCCTCGTGACCACTTCGCGC 198
QY 193 TACGCGAGCAGACCTTCGTGCACACACCGCCGAGAT-----CCCCGACTTCTTCAAG 246
Db 199 TACGCGCTGAAGTGTCTGCGCGCTACCCCGACCATGAAGCAGCAGCAGTCTTCTCAAG 258
QY 247 CAGAGCTTCCCCGAGGCTTCACTTGGGAGAGAACCCACCTACGAGGACGCGGCAATC 306
Db 259 TCCGCACTGCCGAAGGCTAGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGCAAC 318
QY 307 CTGACGCGCCACGAGACACAGCCTGAGGAGCACTGCTGATCTACTAAGGTGAGGTG 366
Db 319 TACAAGACCGCGCGAGGTGAAGTTCGAGGCGGACACCTGTTGTAACCCGATCGAGCTG 378
QY 367 CACGCGACCAACTTCCCCCGGACGCGCCCTGTATGAAGAAACAAGAGCGCGGCTGGGAG 426
Db 379 AAGGCGATCGACTTCAAGGAGGAGCGGCAACATCTCTGGGCGACAGCTGAGTACACTAC 438
QY 427 CCGAGCAGGAGTGGTGTATCCCGAGAAACCGGCTGTCTGTGGGCGGAGAACTGA 481
Db 439 AACAGCCCAACGCTCTATATCATGTGCGCGCAACAGCAGAGAAACCGCATCAAGGTGA 493

RESULT 12
US-09-316-919-15
; Sequence 15, Application US/09316919
; Patent No. 6469154
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: FLUORESCENT PROTEIN INDICATORS


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; FILE REFERENCE: 07257/073001
; CURRENT APPLICATION NUMBER: US/09/316,919
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-09-316-919-15

Query Match      16.1%; Score 110.6; DB 4; Length 720;
Best Local Similarity 55.2%; Pred. No. 2.7e-14;
Matches 262; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 13 CTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGGAGGGGACCGTGAACGGCCACTAC 72
DB 22 CTGTTTACCGGGGTGTGCCCATCTCTGTTCGAGCTGGACGGGAGCTAAACGGCCACAAG 81
QY 73 TTCAAGTGGAGGGGAGGGGAGCGCAACCGCCCTTTCGCGGACCCAGAGCATGAGATC 132
DB 82 TTCAGCGTGTCCGGCGAGGGGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTC 141
QY 133 CAGTGCACGAGGGGCGCCCTTGCCTTCGCTTCGACATCTTGGCCCCCTGCTGCGAG 192
DB 142 ATCTGCACAC---CGGCAAGCTGCCCTGCGCTGGCCCTGTCGACCACTTCGGC 198
QY 193 TAGCGGACGAGGACCTTCGTGCACACACCGCCGAGAT-----CCCCGACTTCTTCAAG 246
DB 199 TAGCGGCTGAAGTGTCTGCCCGGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAG 258
QY 247 CAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACCCACCTACGAGACGGGGCATC 306
DB 259 TCCGCCATGCCGAGGCTACGTCCAGGAGCGCACATCTTCTTCAAGGACGCGCAAC 318
QY 307 CTGACCGCCACACGAGGACCTTGGAGGGCAACTGCTGTATCTACAAGGTGAAGTG 366
DB 319 TACAAGACCCGCGCGAGGTGAAGTTCGAGGGGACACCTCTGTTGNAACCGCATCGAGCTG 378
QY 367 CACGGACCAACTTCCCGCCGAGCGCCCTGTGTGAAGAACAAAGAGCGGGCTGGAG 426
DB 379 AAGGGCATCGACTTCAAGGAGGACGCGCAACATCTCTGGGCGCAAGCTGGAGTACAAC 438
QY 427 CCAGCAGCAGGAGTGTGTACCCCGAGAACGCGTGTCTGCGGCGGAACTGA 481
DB 439 AACAGCCACACGCTATATATCATGCCCAGACAGCAGACGCGCATCAAGTGA 493

RESULT 13
US-09-602-641-14
; Sequence 14, Application US/09602641
; Patent No. 6608189
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; APPLICANT: Lilopis, Juan
; APPLICANT: Wachter, Rebekka M.
; APPLICANT: Remington, S. James
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; FILE REFERENCE: 07257/071001
; CURRENT APPLICATION NUMBER: US/09/602,641
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/172,063
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
; NAME/KEY: misc_feature

; LOCATION: (0)...(0)
; OTHER INFORMATION: EYFP-V68L/Q69K
US-09-602-641-14

Query Match      16.1%; Score 110.6; DB 4; Length 720;
Best Local Similarity 55.2%; Pred. No. 2.7e-14;
Matches 262; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 13 CTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGGAGGGGACCGTGAACGGCCACTAC 72
DB 22 CTGTTTACCGGGGTGTGCCCATCTCTGTTCGAGCTGGACGGGAGCTAAACGGCCACAAG 81
QY 73 TTCAAGTGGAGGGGAGGGGAGCGCAACCGCCCTTTCGCGGACCCAGAGCATGAGATC 132
DB 82 TTCAGCGTGTCCGGCGAGGGGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTC 141
QY 133 CAGTGCACGAGGGGCGCCCTTGCCTTCGCTTCGACATCTTGGCCCCCTGCTGCGAG 192
DB 142 ATCTGCACAC---CGGCAAGCTGCCCTGCGCTGGCCCTGTCGACCACTTCGGC 198
QY 193 TAGCGGACGAGGACCTTCGTGCACACACCGCCGAGAT-----CCCCGACTTCTTCAAG 246
DB 199 TAGCGGCTGAAGTGTCTGCCCGGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAG 258
QY 247 CAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACCCACCTACGAGACGGGGCATC 306
DB 259 TCCGCCATGCCGAGGCTACGTCCAGGAGCGCACATCTTCTTCAAGGACGCGCAAC 318
QY 307 CTGACCGCCACACGAGGACCTTGGAGGGCAACTGCTGTATCTACAAGGTGAAGTG 366
DB 319 TACAAGACCCGCGCGAGGTGAAGTTCGAGGGGACACCTCTGTTGNAACCGCATCGAGCTG 378
QY 367 CACGGACCAACTTCCCGCCGAGCGCCCTGTGTGAAGAACAAAGAGCGGGCTGGAG 426
DB 379 AAGGGCATCGACTTCAAGGAGGACGCGCAACATCTCTGGGCGCAAGCTGGAGTACAAC 438
QY 427 CCAGCAGCAGGAGTGTGTACCCCGAGAACGCGTGTCTGCGGCGGAACTGA 481
DB 439 AACAGCCACACGCTATATATCATGCCCAGACAGCAGACGCGCATCAAGTGA 493

RESULT 14
US-09-316-920A-15
; Sequence 15, Application US/09316920A
; Patent No. 669687
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGN1470
; CURRENT APPLICATION NUMBER: US/09/316,920A
; CURRENT FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-09-316-920A-15

Query Match      16.1%; Score 110.6; DB 4; Length 720;
Best Local Similarity 55.2%; Pred. No. 2.7e-14;
Matches 262; Conservative 0; Mismatches 204; Indels 9; Gaps 2;

QY 13 CTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGGAGGGGACCGTGAACGGCCACTAC 72
DB 22 CTGTTTACCGGGGTGTGCCCATCTCTGTTCGAGCTGGACGGGAGCTAAACGGCCACAAG 81
QY 73 TTCAAGTGGAGGGGAGGGGAGCGCAACCGCCCTTTCGCGGACCCAGAGCATGAGATC 132
DB 82 TTCAGCGTGTCCGGCGAGGGGAGGGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTC 141
QY 133 CAGTGCACGAGGGGCGCCCTTGCCTTCGCTTCGACATCTTGGCCCCCTGCTGCGAG 192
DB 142 ATCTGCACAC---CGGCAAGCTGCCCTGCGCTGGCCCTGTCGACCACTTCGGC 198
QY 193 TAGCGGACGAGGACCTTCGTGCACACACCGCCGAGAT-----CCCCGACTTCTTCAAG 246
DB 199 TAGCGGCTGAAGTGTCTGCCCGGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAG 258
QY 247 CAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACCCACCTACGAGACGGGGCATC 306
DB 259 TCCGCCATGCCGAGGCTACGTCCAGGAGCGCACATCTTCTTCAAGGACGCGCAAC 318
QY 307 CTGACCGCCACACGAGGACCTTGGAGGGCAACTGCTGTATCTACAAGGTGAAGTG 366
DB 319 TACAAGACCCGCGCGAGGTGAAGTTCGAGGGGACACCTCTGTTGNAACCGCATCGAGCTG 378
QY 367 CACGGACCAACTTCCCGCCGAGCGCCCTGTGTGAAGAACAAAGAGCGGGCTGGAG 426
DB 379 AAGGGCATCGACTTCAAGGAGGACGCGCAACATCTCTGGGCGCAAGCTGGAGTACAAC 438
QY 427 CCAGCAGCAGGAGTGTGTACCCCGAGAACGCGTGTCTGCGGCGGAACTGA 481
DB 439 AACAGCCACACGCTATATATCATGCCCAGACAGCAGACGCGCATCAAGTGA 493
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133	QY	CACGTGACGAGGGCGCCCCCTGCGCTTCGACATCTGGCCCCCTGCTGCGAG	192
142	Db	ATCTGCACAC---CGGCAAGCTGCGCTGGGCCACCTCGTGACCACTTCGCG	198
193	QY	TACGGCAGCAGGACTTCGTGCACACACGCGCGAGAT-----CCCGACATCTTCAAG	246
199	Db	TACGGCCTGAAGTGCTTCGCCGGTACCCGACACATGAAGCAGCAGACTTCTCAAG	258
247	QY	CAGAGTTCCCGAGGGTTTCACTGGGAGAGACCACTTACGAGAGCGCGGCATC	306
259	Db	TCGGCATGCGCGAAGGTTACGTCCAGGAGCGCACCTTCTTCAAGGACGACGCGAAC	318
307	QY	CTGACCGGCCACACAGACACCAAGCTTGAGGGCAACTGCGCTGATCTCAAGGTGAAGGTG	366
319	Db	TACAAGACCCGCGCGAGGTGAAGTTCGAGGGGCACACCCTGGTGAACCGCATCGAGCTG	378
367	QY	CAGGCAACCACTTCCCGCGACGGCCCCGTGATGAAGAACGAGAGCGCGCTGGGAG	426
379	Db	AAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAAGCTGGAGTACAACATAC	438
427	QY	CCACGACCGAGGTGGTTAGCCCCGAGAACGGCGTGTGTCGGCCCGGAACCGTGA	481
439	Db	AACAGCCAAACGCTCTATCATGCGCGCAACGAGCAGAAACCGCATCAAGGTGA	493

RESULT 15

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US-09/459-956-2
; Sequence 2, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, iii, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANOUS
; FILE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2

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Query Match	16.0%;	Score 109.8;	DB 3;	Length 690;
Best Local Similarity	57.0%;	Pred. No. 3.9e-14;		
Matches 223;	Conservative 0;	Mismatches 162;	Indels 6;	Gaps 1;
QY	44	ACATGGAGGGACCGTGNACGGCCACTTACTTCAAGTCGAGGCGAGGCGACGGCACC	103	
Db	50	ATATGGATGGGTGTGTCATGGGCAATTACTTTACCGTCAAGGTGAAGGCACACGGGAAGC	109	
QY	104	CCTTCGCGCGCACCCAGAGCATGAG-----AATCCACGTGACCGAGGCGCGCCCGCTGC	157	
Db	110	CATACGAGGAGACGACAGCTTCGACTTTTAAAGTCACCATGGCCAAACGGTGGGCCCTTG	169	
QY	158	CCTTCGCTTCGACATGCTGGCCCGCTGTGCGAGTACGCGACGAGGACCTTTCGTGCACC	217	
Db	170	CATTCTCCTTTGACATACTATCTACAGTGTTCAAATATGAAATCGATGCTTTACTGCGT	229	
QY	218	ACACCGCGAGATCCCGCACTTCTTCAAGCAGAGCTTCCCGGAGGCTTCACCTGGGAGA	277	
Db	230	ATCTTACCAGTATGCCCGACTATTTTCAAACAAGCAATTTCTCTGACGGAATGTCATATGAA	289	
QY	278	GAAACACCACCTTACGAGGACGGCGGCACTCCTGACCGGCCACCAGGACACCAAGCCTTGAGG	337	

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OM nucleic - nucleic search, using sw model

Run on: December 10, 2004, 17:42:24 ; Search time 603 Seconds
(without alignments)
6281.573 Million cell updates/sec

Title: US-09-976-673-11

Perfect score: 687

Sequence: 1 atggtgagcgcctgtgaa.....tgcccgagaaggaactga 687

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4085731 seqs, 2756760397 residues

Total number of hits satisfying chosen parameters: 8171462

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	687	100.0	687	9	US-09-976-673-11
2	671	97.7	687	9	US-09-976-673-11
3	671	97.7	1396	9	US-09-976-673-15
4	671	97.7	1396	18	US-10-806-930-1
5	669.4	97.4	1424	9	US-09-976-673-17
6	669.4	97.4	1424	18	US-10-806-930-3
7	583	84.9	649	17	US-10-439-262-12
8	446.6	65.0	1376	18	US-10-806-930-5
9	441.2	64.2	681	9	US-09-976-673-7
10	438.6	64.0	681	9	US-09-976-673-9
11	438.2	63.8	684	9	US-09-976-673-23
12	436.6	63.6	684	9	US-09-976-673-5

13	436.6	63.6	760	14	US-10-155-809-7
14	436.6	63.6	760	14	US-10-155-809-15
15	435	63.3	910	9	US-09-976-673-1
16	431.8	62.9	760	14	US-10-155-809-9
17	431.8	62.9	760	14	US-10-155-809-11
18	431.8	62.9	760	14	US-10-155-809-13
19	431.8	62.9	908	9	US-09-976-673-3
20	429.2	62.5	680	9	US-09-976-673-25
21	424.8	61.8	696	17	US-10-724-178-17
22	423.2	61.6	699	13	US-10-006-922-41
23	417.8	60.8	707	13	US-10-006-922-39
24	417.8	60.8	707	14	US-10-081-864-21
25	417.8	60.8	1398	18	US-10-806-930-9
26	415.6	60.5	1404	18	US-10-806-930-7
27	396.8	57.8	654	14	US-10-081-864-23
28	372.4	54.2	555	17	US-10-724-178-1064
29	354.6	51.6	591	17	US-10-724-178-1046
30	346.8	50.5	504	17	US-10-724-178-1060
31	324.6	47.2	456	17	US-10-724-178-1052
32	306	44.5	675	17	US-10-724-178-15
33	306	44.5	678	14	US-10-121-258-9
34	299	43.5	713	17	US-10-311-030-11
35	299	43.5	713	17	US-10-311-030-12
36	298.8	43.5	681	17	US-10-311-030-8
37	298.2	43.4	681	14	US-10-121-258-7
38	297.4	43.3	723	14	US-10-152-296-1
39	297.4	43.3	723	17	US-10-724-178-1040
40	295.8	43.1	549	17	US-10-724-178-1036
41	295.2	43.0	504	17	US-10-724-178-1036
42	293	42.6	7508	17	US-10-743-828-4
43	292.4	42.6	678	14	US-10-081-864-7
44	292.4	42.6	678	15	US-10-315-920-1
45	292.4	42.6	678	15	US-10-315-920-3

ALIGNMENTS

RESULT 1

US-09-976-673-11
; Sequence 11, Application US/099766673
; Patent No. US20020160473A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Pradkov, Arcady
; APPLICANT: Labas, Yulii
; APPLICANT: Matz, Mikhail
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Gurskaya, Nadezda
; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS
; FILE REFERENCE: CLON-028WO
; CURRENT APPLICATION NUMBER: US/09/976,673
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,018
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60,306,131
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 687
; TYPE: DNA
; ORGANISM: heteractis crispa
US-09-976-673-11

Query Match 100.0%; Score 687; DB 9; Length 687;

Best Local Similarity 100.0%; Pred. No. 6.9e-167;

Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTACGGCGCTGCTGAGGAGGATATCCCATCAAGATGATGATGAGGCGCCCGTG 60

Db 1 ATGGTACGGCGCTGCTGAGGAGGATATGCGCATCAAGATGATGATGAGGCGCCCGTG 60

QY 61 AACGCCCACTACTTCAAGTGGAGGGGAGGGGAGCGCAACCCCTTTCGGCGGACCCAG 120
DB 61 AACGCCCACTACTTCAAGTGGAGGGGAGGGGAGCGCAACCCCTTTCGGCGGACCCAG 120
QY 121 AGCATGAGATCCAGTACCGAGGGGCGCCCTTTCGGCTTTCGACATCCTGGCC 180
DB 121 AGCATGAGATCCAGTACCGAGGGGCGCCCTTTCGGCTTTCGACATCCTGGCC 180
QY 181 CCCTCTCGAGTACGGCAGCAGACCTTCGTGACCAACACCGCGGAGATCCCGACTTC 240
DB 181 CCCTCTCGAGTACGGCAGCAGACCTTCGTGACCAACACCGCGGAGATCCCGACTTC 240
QY 241 TTCAAGCAGAGCTTCCCGAGGGCTTCACTTGGAGAGAACCAACCTTACGAGGACGGC 300
DB 241 TTCAAGCAGAGCTTCCCGAGGGCTTCACTTGGAGAGAACCAACCTTACGAGGACGGC 300
QY 301 GGCATCTCTGACCGCCACAGGACACAGCCTTGGAGGGCAACTGCCTGATCTCAAGGTG 360
DB 301 GGCATCTCTGACCGCCACAGGACACAGCCTTGGAGGGCAACTGCCTGATCTCAAGGTG 360
QY 361 AAGTGTGACGACCAACTTCCCGCGACCGGCGCCCTTTCGATGAGAAACAGAGCGGCGC 420
DB 361 AAGTGTGACGACCAACTTCCCGCGACCGGCGCCCTTTCGATGAGAAACAGAGCGGCGC 420
QY 421 TGGAGGCCAGCAGCAGGAGTGTGTACCCCGAGAACCGCGTGTGTGGCGCGGAACTG 480
DB 421 TGGAGGCCAGCAGCAGGAGTGTGTACCCCGAGAACCGCGTGTGTGGCGCGGAACTG 480
QY 481 ATGGCCCTGAAGTGGGCGACCGGCACTGTATCTGCCACCACTACAGAGTACCGGAGC 540
DB 481 ATGGCCCTGAAGTGGGCGACCGGCACTGTATCTGCCACCACTACAGAGTACCGGAGC 540
QY 541 AAGAGGCCGTGGCGCCCTGACCATGCGCGCTTCCACTTACCGACATCCGCTCCAG 600
DB 541 AAGAGGCCGTGGCGCCCTGACCATGCGCGCTTCCACTTACCGACATCCGCTCCAG 600
QY 601 ATGCTGCGGAAGAAGAGGAGTACTTCAGCTGTACGAGGCGAGCTGGCCCGGTAC 660
DB 601 ATGCTGCGGAAGAAGAGGAGTACTTCAGCTGTACGAGGCGAGCTGGCCCGGTAC 660
QY 661 ACCGACCTGCCCGAGAGGCCCACTGA 687
DB 661 ACCGACCTGCCCGAGAGGCCCACTGA 687

RESULT 2

US-09-976-673-13
; Sequence 13, Application US/09976673
; Patent No. US20020160473A1
; GENERAL INFORMATION:
; APPLICANT: Lukanov, Sergey
; APPLICANT: Pradkov, Arcady
; APPLICANT: Labas, Yulii
; APPLICANT: Matz, Mikhail
; APPLICANT: Lukanov, Konstantin
; APPLICANT: Gurskaya, Nadezda
; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS
; FILE REFERENCE: CLON-028WO
; CURRENT APPLICATION NUMBER: US/09/976,673
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,018
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60,306,131
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 687
; TYPE: DNA
; ORGANISM: heteractis crisp
US-09-976-673-13

Query Match

97.7%; Score 671; DB 9; Length 687;

Best Local Similarity 98.5%; Pred. No. 8.9e-163;
Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGCTGAGCGGCTCTCAAGGAGAGTATGGGATCAAGATGTATCATGGAGGACCGGTG 60
DB 1 ATGCTGAGCGGCTCTCAAGGAGAGTATGGGATCAAGATGTATCATGGAGGACCGGTG 60
QY 61 AACGCCCACTACTTCAAGTGGAGGGGAGGGGAGCGCAACCCCTTTCGGCGGACCCAG 120
DB 61 AACGCCCACTACTTCAAGTGGAGGGGAGGGGAGCGCAACCCCTTTCGGCGGACCCAG 120
QY 121 AGCATGAGATCCAGTACCGAGGGGCGCCCTTTCGGCTTTCGACATCCTGGCC 180
DB 121 AGCATGAGATCCAGTACCGAGGGGCGCCCTTTCGGCTTTCGACATCCTGGCC 180
QY 181 CCCTCTCGAGTACGGCAGCAGACCTTCGTGACCAACACCGCGGAGATCCCGACTTC 240
DB 181 CCCTCTCGAGTACGGCAGCAGACCTTCGTGACCAACACCGCGGAGATCCCGACTTC 240
QY 241 TTCAAGCAGAGCTTCCCGAGGGCTTCACTTGGAGAGAACCAACCTTACGAGGACGGC 300
DB 241 TTCAAGCAGAGCTTCCCGAGGGCTTCACTTGGAGAGAACCAACCTTACGAGGACGGC 300
QY 301 GGCATCTCTGACCGCCACAGGACACAGCCTTGGAGGGCAACTGCCTGATCTCAAGGTG 360
DB 301 GGCATCTCTGACCGCCACAGGACACAGCCTTGGAGGGCAACTGCCTGATCTCAAGGTG 360
QY 361 AAGTGTGACGACCAACTTCCCGCGACCGGCGCCCTTTCGATGAGAAACAGAGCGGCGC 420
DB 361 AAGTGTGACGACCAACTTCCCGCGACCGGCGCCCTTTCGATGAGAAACAGAGCGGCGC 420
QY 421 TGGAGGCCAGCAGCAGGAGTGTGTACCCCGAGAACCGCGTGTGTGGCGCGGAACTG 480
DB 421 TGGAGGCCAGCAGCAGGAGTGTGTACCCCGAGAACCGCGTGTGTGGCGCGGAACTG 480
QY 481 ATGGCCCTGAAGTGGGCGACCGGCACTGTATCTGCCACCACTACAGAGTACCGGAGC 540
DB 481 ATGGCCCTGAAGTGGGCGACCGGCACTGTATCTGCCACCACTACAGAGTACCGGAGC 540
QY 541 AAGAGGCCGTGGCGCCCTGACCATGCGCGCTTCCACTTACCGACATCCGCTCCAG 600
DB 541 AAGAGGCCGTGGCGCCCTGACCATGCGCGCTTCCACTTACCGACATCCGCTCCAG 600
QY 601 ATGCTGCGGAAGAAGAGGAGTACTTCAGCTGTACGAGGCGAGCTGGCCCGGTAC 660
DB 601 ATGCTGCGGAAGAAGAGGAGTACTTCAGCTGTACGAGGCGAGCTGGCCCGGTAC 660
QY 661 ACCGACCTGCCCGAGAGGCCCACTGA 687
DB 661 ACCGACCTGCCCGAGAGGCCCACTGA 687

RESULT 3

US-09-976-673-15
; Sequence 15, Application US/09976673
; Patent No. US20020160473A1
; GENERAL INFORMATION:
; APPLICANT: Lukanov, Sergey
; APPLICANT: Pradkov, Arcady
; APPLICANT: Labas, Yulii
; APPLICANT: Matz, Mikhail
; APPLICANT: Lukanov, Konstantin
; APPLICANT: Gurskaya, Nadezda
; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS
; FILE REFERENCE: CLON-028WO
; CURRENT APPLICATION NUMBER: US/09/976,673
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,018
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60,306,131
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion construct
US-09-976-673-15

Query Match 97.7%; Score 671; DB 9; Length 1396;
Best Local Similarity 98.5%; Pred. No. 9.3e-163;
Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	1	ATGGTGAGCGGCGCTGCTGAAGGAGAGTATGGCATCAAGATGTACATGGAGGACACCGTG	60
DB	710	ATGGTGAGCGGCGCTGCTGAAGGAGAGTATGGCATCAAGATGTACATGGAGGACACCGTG	769
QY	61	AACGGCCACTACTTTCAAGTGGAGGGCGAGGGCGAAGCGCAACCCCTTCGCGGACACCGAG	120
DB	770	AACGGCCACTACTTTCAAGTGGAGGGCGAGGGCGAAGCGCAACCCCTTCGCGGACACCGAG	829
QY	121	ACCATGAGAAATCAGCTGACCGAGGGCGCCCTGCGCCCTTCGCTTCGCATCTCGATCTGGCC	180
DB	830	ACCATGAGAAATCAGCTGACCGAGGGCGCCCTGCGCCCTTCGCTTCGCATCTCGATCTGGCC	889
QY	181	CCCTGCTGCGAGTACGGCAGCAGGACCTTCGTCACACACACCGCGAGATCCCGACTTC	240
DB	890	CCCTGCTGCGAGTACGGCAGCAGGACCTTCGTCACACACACCGCGAGATCCCGACTTC	949
QY	241	TTCAAGCAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACACACCTACGAGGACGGC	300
DB	950	TTCAAGCAGAGCTTCCCGAGGGCTTACCTGGGAGAGAACACACCTACGAGGACGGC	1009
QY	301	GGCATCCTCAACCGCCACACGAGCACCAGCTCGTCACACACACCGCGAGATCCCGACTTC	360
DB	1010	GGCATCCTCAACCGCCACACGAGCACCAGCTCGTCACACACACCGCGAGATCCCGACTTC	1069
QY	361	AGGTGACGGCACCAACTTTCGCCCGAAGCGGCGGCTGATGAAGAACAGAGCGGCGGC	420
DB	1070	AGGTGACGGCACCAACTTTCGCCCGAAGCGGCGGCTGATGAAGAACAGAGCGGCGGC	1129
QY	421	TGGGAGCCGACGACGAGTGGTACCCCGAGAACCGCGTGTGTGGCGCGGACCGT	480
DB	1130	TGGGAGCCGACGACGAGTGGTACCCCGAGAACCGCGTGTGTGGCGCGGACCGT	1189
QY	481	ATGGGCCCTGAAGGTGGGCGACGGCACCTGATCTGCCACCACTACACAGCTACCGGAGC	540
DB	1190	ATGGGCCCTGAAGGTGGGCGACGGCACCTGATCTGCCACCACTACACAGCTACCGGAGC	1249
QY	541	AGAAGGCGGTGCGCGCCCTGACCATGCGCGGCTTCACCTACCGACATCCGGCTCCAG	600
DB	1250	AGAAGGCGGTGCGCGCCCTGACCATGCGCGGCTTCACCTACCGACATCCGGCTCCAG	1309
QY	601	ATGCTGCGGAAGAAGAAGCAGTACTTTCAGTGTACGAGGCGCAGCGTGGCGCGGTAC	660
DB	1310	ATGCTGCGGAAGAAGAAGCAGTACTTTCAGTGTACGAGGCGCAGCGTGGCGCGGTAC	1369
QY	661	AGCGACCTGCGCGGAGAGGCCAACTGA	687
DB	1370	AGCGACCTGCGCGGAGAGGCCAACTGA	1396

RESULT 4
US-10-806-930-1
; Sequence 1, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; TITLE OF INVENTION: Nucleic Acids Encoding Linked
; TITLE OF INVENTION: Chromo/Fluorescent Domains and Methods for Using the Same
; FILE REFERENCE: CLON-094
; CURRENT APPLICATION NUMBER: US/10/806,930
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/976,673

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/ INVENTION: Nucleic Acids Encouraging Linked
/ TITLE OF INVENTION: Chromo-Fluorescent Domains and Methods for Using the Same
/ FILE REFERENCE: CLON-094
/ CURRENT APPLICATION NUMBER: US/10/806,930
/ CURRENT FILING DATE: 2004-03-22
/ PRIOR APPLICATION NUMBER: 09/976,673
/

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; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/356,225
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/383,336
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/32560
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1396
; TYPE: DNA
; ORGANISM: Anthozoa
US-10-806-930-1

Query Match          97.7%; Score 671; DB 18; Length 1396;
Best Local Similarity 98.5%; Pred. No. 9.3e-163;
Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGCTGAGCGGCTGCTGAAGGAGAGATGTCGCATCAAGATGTACATGGAGGCGACCGTG 60
DB 710 ATGCTGAGCGGCTGCTGAAGGAGAGATGCGCATCAAGATGTACATGGAGGCGACCGTG 769

QY 61 AACGGCCACTACTTCAAGTGCAGGGCGAGGGCGAGCGCAACCCCTTCGCGGCACCCAG 120
DB 770 AACGGCCACTACTTCAAGTGCAGGGCGAGGGCGAGCGCAACCCCTTCGCGGCACCCAG 829

QY 121 AGCATGAGATCCAGTACCGAGGGGCGCCCCCTTGCCTTCGNATCTCTGGCC 180
DB 830 AGCATGCGGATCACGTGACCGAGGGGCGCCCCCTTGCCTTCGCATCTCTGGCC 889

QY 181 CCCTGCTGCGAGTACGGCAGCAGCACTTCGTGCACACACCGCCGAGATCCCGCACTTC 240
DB 890 CCCTGCTGCGAGTACGGCAGCAGCACTTCGTGCACACACCGCCGAGATCCCGCACTTC 949

QY 241 TTCAAGAGAGCTTCCCGAGGGCTTCACTTGGGAGAGAACCACTTACGAGGACGGC 300
DB 950 TTCAAGCAGAGCTTCCCGAGGGCTTCACTTGGGAGAGAACCACTTACGAGGACGGC 1009

QY 301 GGCATCTGACCGCCACACAGGACACAGAGCTTGGAGGGCAACTGCTGTACTACAAGTG 360
DB 1010 GGCATCTGACCGCCACACAGGACACAGAGCTTGGAGGGCAACTGCTGTACTACAAGTG 1069

QY 361 AAGGTGCACGGCACCAACTTCCCGCGACGGCCCCGTGATGAAGAACCAAGACGGCGGC 420
DB 1070 AAGGTGCTGGGCACCAACTTCCCGCGACGGCCCCGTGATGAAGAACCAAGACGGCGGC 1129

QY 421 TGGAGGCCNAGCACGAGGTGTTACCCCGAGAGAGCGGTGCTGTGCGGCCGAGAGTG 480
DB 1130 TGGAGGCCNAGCACGAGGTGTTACCCCGAGAGAGCGGTGCTGTGCGGCCGAGAGTG 1189

QY 481 ATGCGCCCTGAAGGTGGGCGCACCGGCACCTGTACTGTGCACCACTTACACCACTACCGGAGC 540
DB 1190 ATGCGCCCTGAAGGTGGGCGCACCGGCGGCTGTACTGTGCACCACTTACACCACTACCGGAGC 1249

QY 541 AAGAAGCGCTGCGCGCCCTGACATGCGCGGCTTCCACTTCAACCGACATCCGGCTCCAG 600
DB 1250 AAGAAGCGCTGCGCGCCCTGACATGCGCGGCTTCCACTTCAACCGACATCCGGCTCCAG 1309

QY 601 ATGCTCGGAAGAAGAGGACAGTAGTCTTCGAGCTGTACGAGGCCAGCGTGGCCCCGGTAC 660
DB 1310 ATGCTCGGAAGAAGAGGACAGTAGTCTTCGAGCTGTACGAGGCCAGCGTGGCCCCGGTAC 1369

QY 661 AGCGACTGCCCCGAGAAGGCCCACTGA 687
DB 1370 AGCGACTGCCCCGAGAAGGCCCACTGA 1396

RESULT 5
US-09-976-673-17
; Sequence 17, Application US/09976673
; Patent No. US20020160473A1
; GENERAL INFORMATION:

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RESULT 5
US-09-976-673-17
; Sequence 17, Application US/09976673
; Patent No. US20020160473A1
; GENERAL INFORMATION:

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; APPLICANT: Lukanov, Sergey
; APPLICANT: Pradkov, Arcady
; APPLICANT: Labas, Yulii
; APPLICANT: Matz, Mikhail
; APPLICANT: Lukanov, Konstantin
; APPLICANT: Gurskaya, Nadezda
; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS
; FILE REFERENCE: CLON-028WO
; CURRENT APPLICATION NUMBER: US/09/976,673
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,018
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/306,131
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion construct
US-09-976-673-17

Query Match          97.4%; Score 669.4; DB 9; Length 1424;
Best Local Similarity 98.4%; Pred. No. 2.4e-162;
Matches 676; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGTGAGCGGCTGCTCAAGAGAGATGCGCATCAAGATGTACATGGAGGACCGTG 60
DB 14 ATGTGAGCGGCTGCTCAAGAGAGATGCGCATCAAGATGTACATGGAGGACCGTG 73
QY 61 AACGGCCACTACTTCAAGTGGAGGCGAGGCGACCGCAACCCCTTCGGCGGACCCAG 120
DB 74 AACGGCCACTACTTCAAGTGGAGGCGAGGCGACCGCAACCCCTTCGGCGGACCCAG 133
QY 121 AGCATGAGAAATCCACGTGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 134 AGCATGCGGATCCACGTGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 193
QY 181 CCCTGCTCGAGTACGGCAGCAGACCTTCGTGACACACCGCGGAGATCCCGACTTC 240
DB 194 CCCTGCTCGAGTACGGCAGCAGACCTTCGTGACACACCGCGGAGATCCCGACTTC 253
QY 241 TTCAAGCAGAGCTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 300
DB 254 TTCAAGCAGAGCTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 313
QY 301 GGCATCTGACCGGCCACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 360
DB 314 GGCATCTGACCGGCCACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 373
QY 361 AAGGTGACCGGACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 420
DB 374 AAGGTGACCGGACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 433
QY 421 TGGGAGCCAGCAGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 480
DB 434 TGGGAGCCAGCAGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 493
QY 481 ATGGCCCTGAGGTGGGCGACCGGCGACCTGATCTGCCACCACTACACGAGTACCGGAGC 540
DB 494 ATGGCCCTGAGGTGGGCGACCGGCGACCTGATCTGCCACCACTACACGAGTACCGGAGC 553
QY 541 AAGAGGCGGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 600
DB 554 AAGAGGCGGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 613
QY 601 ATGTGCGGAGAGAGAGAGAGTACTTCCAGCTGTACGAGGCGGCGGCGGCGGCGG 660
DB 614 ATGTGCGGAGAGAGAGAGAGTACTTCCAGCTGTACGAGGCGGCGGCGGCGGCGG 673
QY 661 AGCGACCTGCGGCGGAGAGAGAGTACTTCCAGCTGTACGAGGCGGCGGCGGCGG 687
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DB 674 AGCGACCTGCGGCGGAGAGGCGCAACAGA 700
|||||
RESULT 6
US-10-806-930-3
; Sequence 3, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukanov, Sergey
; TITLE OF INVENTION: Nucleic Acids Encoding Linked
; Chromo/Fluorescent Domains and Methods for Using the Same
; FILE REFERENCE: CLON-094
; CURRENT APPLICATION NUMBER: US/10/806,930
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/356,225
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/383,336
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/32560
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Anthozoa
US-10-806-930-3

Query Match          97.4%; Score 669.4; DB 18; Length 1424;
Best Local Similarity 98.4%; Pred. No. 2.4e-162;
Matches 676; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGTGAGCGGCTGCTCAAGAGAGATGCGCATCAAGATGTACATGGAGGACCGTG 60
DB 14 ATGTGAGCGGCTGCTCAAGAGAGATGCGCATCAAGATGTACATGGAGGACCGTG 73
QY 61 AACGGCCACTACTTCAAGTGGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 74 AACGGCCACTACTTCAAGTGGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 133
QY 121 AGCATGAGAAATCCACGTGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
DB 134 AGCATGCGGATCCACGTGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 193
QY 181 CCCTGCTCGAGTACGGCAGCAGACCTTCGTGACACACCGCGGAGATCCCGACTTC 240
DB 194 CCCTGCTCGAGTACGGCAGCAGACCTTCGTGACACACCGCGGAGATCCCGACTTC 253
QY 241 TTCAAGCAGAGCTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 300
DB 254 TTCAAGCAGAGCTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 313
QY 301 GGCATCTGACCGGCCACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 360
DB 314 GGCATCTGACCGGCCACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 373
QY 361 AAGGTGACCGGACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 420
DB 374 AAGGTGACCGGACCACTTCCCGAGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 433
QY 421 TGGGAGCCAGCAGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 480
DB 434 TGGGAGCCAGCAGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 493
QY 481 ATGGCCCTGAGGTGGGCGACCGGCGACCTGATCTGCCACCACTACACGAGTACCGGAGC 540
DB 494 ATGGCCCTGAGGTGGGCGACCGGCGACCTGATCTGCCACCACTACACGAGTACCGGAGC 553
QY 541 AAGAGGCGGCGGCGCTTCCACCATGCGGCGTTCACCTGGGAGAGAACCCACCTACGAGGCGGC 600
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Db 554 AAGAAAGCGCGCTGACCATGCGCGCTTCCACTTACCGACATCCGGCTGCAG 613
QY 601 ATGCTGGGAGAGAGAGGAGTACTTCCAGCTGTACGAGCCAGCGTGGCCCGGTAC 660
Db 614 ATGCTGGGAGAGAGAGGAGTACTTCCAGCTGTACGAGCCAGCGTGGCCCGGTAC 673
QY 661 AGCAGCTGCGCGGAGAGGCGCAACTGA 687
Db 674 AGCAGCTGCGCGGAGAGGCGCAACAGA 700

RESULT 7
US-10-439-262-12
; Sequence 12, Application US/10439262
; Publication No. US20040106566A1
; GENERAL INFORMATION:
; APPLICANT: LIN, Shi-Lung
; TITLE OF INVENTION: RNA-Splicing and Processing-Directed
; ; Gene Silencing and The Relative Applications Thereof
; ;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIN, Shi-Lung
; STREET: 1953 Wellesley Road,
; CITY: San Marino
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/439,262
; FILING DATE: 15-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/391,651
; FILING DATE: 17-MAY-2002
; APPLICATION NUMBER: US 60/411,062
; FILING DATE: 16-SEP-2002
; APPLICATION NUMBER: US 60/418,405
; FILING DATE: 12-OCT-2002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626)289-7172
; TELEFAX: (323)442-3158
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 649 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: mutated red fluorescent protein (rGFP) gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-439-262-12

Query Match 84.9%; Score 583; DB 17; Length 649;
Best Local Similarity 93.8%; Pred. No. 3.6e-140;
Matches 646; Conservative 0; Mismatches 0; Indels 43; Gaps 2;
QY 1 ATGGTGGCGGCTGCTGAAGAGAGTATGCGCATCAAGATGTACATGGAGGCGACCGTG 60
Db 1 ATGGTGGCGGCTGCTGAAGAGAGTATGCGCATCAAGATGTACATGGAGGCGACCGTG 60
QY 61 AACGGCCACTACTTCAAGTGGAGGCGGAGGCGGAGCGGCAACCCCTTCGCGGCAACCCAG 120
Db 61 AACGGCCACTACTTCAAGTGGAGGCGGAGGCGGAGCGGCAACCCCTTCGCGGCAACCCAG 120

QY 121 AGCATGAGAATCCAGTGAACGAGGCGCCCCCTTGCCTTTCGATCTCGACATCTCGCC 180
Db 121 AGCATGAGAATCCAGTGAACGAGGCGCCCCCTTGCCTTTCGATCTCGACATCTCGCC 180
QY 181 CCTCTCTGGAGTACGGCAGCAG---GACCTTCGTGACACACCGCGGAGATCCCGAC 237
Db 181 CCTCTCTGGAGTACGGCAGCAGCAGCCTTCGTGACACACCGCGGAGATCCCGAC 240
QY 238 TTCTTCAAGCAGAGCTTCCCCGAGGGCTTACCTGGGAGAGAACCCACCCTTACGAGAC 297
Db 241 TTCTTCAAGCAGAGCTTCCCCGAGGGCTTACCTGGGAG----- 279
QY 298 GCGGGATCTGACCGCCCAACAGACACACCGCTTGGAGGGCACTGCTGATCTACAAG 357
Db 280 -----ACCAGACACACCGCTTGGAGGGCACTGCTGATCTACAAG 320
QY 358 GTGAAGGTGACGCGCAACCACTTCCCCCGCGAGCGCCCGCTGATGAAGAACAAAGAGCGGC 417
Db 321 GTGAAGGTGACGCGCAACCACTTCCCCCGCGAGCGCCCGCTGATGAAGAACAAAGAGCGGC 380
QY 418 GGTGGAGCGCCAGCAGCAGGTGTGTACCCCGAGAGAGCGGCTGTGTGGCGCGGAAAC 477
Db 381 GGTGGAGCGCCAGCAGCAGGTGTGTACCCCGAGAGAGCGGCTGTGTGGCGCGGAAAC 440
QY 478 GTGATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCTACACCACTACCGG 537
Db 441 GTGATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCTACACCACTACCGG 500
QY 538 AGCAAGAAGCGCGTGGCGCCCTGACCAATGCGCGCTTCCATTACCGACATCCGGCTC 597
Db 501 AGCAAGAAGCGCGTGGCGCCCTGACCAATGCGCGCTTCCATTACCGACATCCGGCTC 560
QY 598 CAGATCTCGGAGAGAGAGGAGGAGGAGTACTTTCGAGCTGTACGAGGCGGAGCTGGCCCG 657
Db 561 CAGATCTCGGAGAGAGAGGAGGAGGAGTACTTTCGAGCTGTACGAGGCGGAGCTGGCCCG 620
QY 658 TACAGCGACCTGCCCGAGAGGCGCAACTG 686
Db 621 TACAGCGACCTGCCCGAGAGGCGCAACTG 649

RESULT 8
US-10-806-930-5
; Sequence 5, Application US/10806930
; Publication No. US20040216180A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; TITLE OF INVENTION: Nucleic Acids Encoding Linked
; ; Chromo/Fluorescent Domains and Methods for Using the Same
; FILE REFERENCE: CLON-094
; CURRENT APPLICATION NUMBER: US/10/806,930
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/356,225
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/383,336
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: PCT/US02/32560
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Anthozoa
US-10-806-930-5

Query Match 65.0%; Score 446.6; DB 18; Length 1376;
Best Local Similarity 78.2%; Pred. No. 4.2e-105;
Matches 536; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
QY 3 GGTGAGCGGCTGCTGAAGAGAGAGTATGCGCATCAAGATGTACATGGAGGCGACCGTGAA 62

Db 692 GATGCTGCTGTTGTTGAAAGAGATGCGCATCAAGATGTACATGGAAGGCACGGTTAA 751
Qy 63 CGGCCACTACTTCAAGTGGAGGGGAGGGGAGCGGCAACCCCTTCGCGGACACCGAG 122
Db 752 TGGCCATTATTTCAAGTGTGAAGGAGGAGGAGCGGCAACCCATTTGAGGATGCGAGAG 811
Qy 123 CATGAGATPCCACGTGACCGAGGGGCGCCCTGCGCTTCGCTTCGACATCTCTGGCCCC 182
Db 812 CATGAGATTCATGTCACCGAGGGGCTCCATTACCATTTGCTTCGACATTTGGCACC 871
Qy 183 CTGCTGGAGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
Db 872 GTGTTGTGAGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 931
Qy 243 CAAGCAGAGCTTCCCGGAGGGGCTTCCACCTGGGAGAGAACCAACCTACGAGGAGCGGG 302
Db 932 CAAGCAGCTTTCCTGAGGCTTTACTTGGGAGAGAACCAACCTATGAGATGAGGAGG 991
Qy 303 CATCTGACCGCCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 362
Db 992 CATCTTACTGCTCATCAGGACACAAAGGCTTGAGGGGAACTGCGCTTATATACAAAGGTCAA 1051
Qy 363 GTGTCACGCGCACCACTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 422
Db 1052 AGTCCATGGTACCAATTTTCTGCTGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1111
Qy 423 GGAGCCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482
Db 1112 GGAGCCAGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1171
Qy 483 GGCCTGAGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 542
Db 1172 GGCCTTAAAGTCGGTGTGCTGATTTATCCAGAGAGTGTGCTGCTGAGGAGGAGGAGGAG 1231
Qy 543 GAAGCCGCTGGGCGGCTTACGATGCGGCTTCCACTTCCAGGAGGAGGAGGAGGAGGAGGAG 602
Db 1232 GAAGCAGTCGCTGCTTGAATGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1291
Qy 603 GCTGCGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 662
Db 1292 GCTGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1351
Qy 663 CGACCTGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 687
Db 1352 TGATCTTCTGAAAGAGCAATTGA 1376

RESULT 9

US-09-976-673-7

; Sequence 7, Application US/09976673

; Patent No. US20020160473A1

; GENERAL INFORMATION:

; APPLICANT: Lukyanov, Sergey

; APPLICANT: Fradkov, Arcady

; APPLICANT: Labas, Yulii

; APPLICANT: Matz, Mikhail

; APPLICANT: Lukyanov, Konstantin

; APPLICANT: Gurskaya, Nadezda

; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS

; FILE REFERENCE: CLON-028W

; CURRENT APPLICATION NUMBER: US/09/976,673

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,018

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 60,306,131

; PRIOR FILING DATE: 2001-07-16

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 681

; TYPE: DNA

; ORGANISM: heteractis crisp

US-09-976-673-7

Query Match 54.2%; Score 441.2; DB 9; Length 681;

Best Local Similarity 78.2%; Pred. No. 9.8e-104;

Matches 530; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 10 GGCTCTCTGAAGGAGATGCGCATCAAGATGTACATGGAAGGCACCGTGAACGGCCAC 69
Db 4 GGTGTTGTTGAAGAGATGCGCATCAAGATGTACATGGAAGGCACCGTGAATGGCCAT 63
Qy 70 TACTTCAAGTGGAGGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 129
Db 64 TATTTCAAGTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 123
Qy 130 ATCCAGCTCACGAGGGGCGCCCTGCGCTTCGCTTCGACATCTTGGCCCCCTGCTGC 189
Db 124 ATTCATGTCACGAGGGGCTCCATTACCATTTGCTTCGACATTTGGCACCGGTGT 183
Qy 190 GAGTACGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 249
Db 184 GAGTACGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Qy 250 AGCTTCCCGGAGGCTTCACTGGGAGAGAACCAACCTACGAGGAGGAGGAGGAGGAGGAG 309
Db 244 TCTTTCCCTGAAGGCTTTACTTGGGAGAGAACCAACCTATGAAGATGGAGGATCTT 303
Qy 310 ACCGCCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 369
Db 304 ACTGCTCATCAGGACACAAAGGCTGGAGGGAACTGCTTATATACAGGTGAAAGTCTT 363
Qy 370 GGCACCAACTTCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 429
Db 364 GGTACCAATTTTCTGCTGATGGCCCCGCTGATGAAGAGAACAAATCAGGAGGATGGAGGCA 423
Qy 430 AGCAGCGAGGTGTGTACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 489
Db 424 AGCAGTGGAGTGTGTTTATCCAGAGAGTGTGCTGTGTGAGCGTAAATGTGATGSCCTT 483
Qy 490 AAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 549
Db 484 AAAGTCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
Qy 550 GTGCGGCGCTTACCATGCGGCTTCCACTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 609
Db 544 GTCCGTGCTTGAATGCCAGGATTTCAATTTTACAGACATCCGCTTCAGATGCTGAGG 603
Qy 610 AAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
Db 604 AAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 663
Qy 670 CCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 687
Db 664 CCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681

RESULT 10

US-09-976-673-9

; Sequence 9, Application US/09976673

; Patent No. US20020160473A1

; GENERAL INFORMATION:

; APPLICANT: Lukyanov, Sergey

; APPLICANT: Fradkov, Arcady

; APPLICANT: Labas, Yulii

; APPLICANT: Matz, Mikhail

; APPLICANT: Lukyanov, Konstantin

; APPLICANT: Gurskaya, Nadezda

; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS

; FILE REFERENCE: CLON-028W

; CURRENT APPLICATION NUMBER: US/09/976,673

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,018

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 60,306,131

Qy	545	AGCCGTGCGCGCTCGACCATGCCCGGTTCCACTTCCGACATCCGACATCCCGCTCCAGATGC	604
Db	618	AACAGTCCGTCGCTTTGACAAATGCCAGGATTTCAATTTACAGACATCCGCTTCAGATGC	677
Qy	605	TGCGGAAGAAAGAACGACGAGTACTTTCGAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCG	664
Db	678	CGAGGAAAAGAAAGACGAGTACTTTGAATGTACGAGCATCTGTGCGCTAGGTACAGTG	737
Qy	665	ACCTGCCCAGGAAGGCCAACTGA	687
Db	738	ATCTTCTGAAAAAGCAAAATTCGA	760

RESULT 14

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US-10-155-809-15
; Sequence 15, Application US/10155809
; Publication No. US20030092884A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Chudakov, Dmitry
; TITLE OF INVENTION: Kindling Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Their Use
; FILE REFERENCE: CLON-073
; CURRENT APPLICATION NUMBER: US/10/155,809
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,752
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/323,176
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/210,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/976,673
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 760
; TYPE: DNA
; ORGANISM: Anthozoa
US-10-155-809-15

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Query Match	63.6%	Score 436.6;	DB 14;	Length 760;
Best Local Similarity	77.5%;	Pred. No. 1.5e-102;		
Matches 529;	Conservative	0;	Mismatches 154;	Indels 0; Gaps 0;

Qy	5	TGAGCGCGCTGCTGTAAGGAGAGTATGCCCATCAAGATGTATCATGAGGGGACCGTGAACG	64
Db	78	TGCGTGGTTTGTGAAGAAAGATATGCGCATCAAGATGTATCATGAAGGACCGGTTAATG	137
Qy	65	GCCACTACTTCAAGTTCGAGGGCGGAGGCGACGCCCTTCGCGGCGACCCAGAGCA	124
Db	138	GCCATTATTTCAAGTGTGNAAGGAGGAGGAGCGCNACCCATTTCAGAGTACGACAGCA	197
Qy	125	TGGAATCCAGGTGACCGGAGGGCGGCCCTTCGCCCTTCGACATCCTGGGCCCGCT	184
Db	198	TGAGGATTCATGTCCACCGAAGGGGCTCCATTACCAATTTCGCTTCGACATTTTGGCACCGT	257
Qy	185	GCTTCGAGTAGTCGGCAGCAGGACCTTCGTGTCACCAACGCGCGAGATCCCCGACTTCTTCA	244
Db	258	GTTGTGAGTACGGCAGCAGGACCTTGTTCACCATTACGGCAGAGATTTCCCGATTCTTCA	317
Qy	245	AGCAGAGCTTCCCGAGGGCTTCACCTCGGAGAGAACCAACCACTACGAGGACGGCGCA	304
Db	318	AGCAGTCTTTCCTGAAGGCTTTACTTGGGAAAGAACCAACCTATGAAGATGAGAGGA	377
Qy	305	TCTGTACGCCCCACGAGACACCGCTTCGAGGGGCAACTGCCTGATCTACAAGGTGAAG	364
Db	378	TTCTTACTGCTCATCAGACACAAGCTTCGAGGGGGACTGCCTTATATACAAGGTGAAG	437

Qy	365	TGCAGCGACCAACTTCCCGCCGACCGCCCGGTGATGAAGAACAGAGACCGCGCGCTGGG	424
Db	438	TCCTTGGTACCAAATTTTCTGCTGATGCGCCCGGTGATGAAGAACAAATCAGAGGATGGG	497
Qy	425	AGCCGAGCACCGAGGTGGTGTACCCCGAGAACGGCGTGCTGTGCGGCCGGAAACGTGATGG	484
Db	498	AGCCAAAGCACTAGGTGGTTTATCCAGAGAATGGTGCTCTGTGTGAGAGTACGCGTGATGG	557
Qy	485	CCCTGAGGTGGGGCAGCGGCACTGATCTGCCACCACTACACAGCTTACCGGAGCAAGA	544
Db	558	CCCTTAAGTCGGTGATCGTCGTTGATCTGCCATCACTATATCTTTCAGGTCCTCAAGA	617
Qy	545	AGGCGGTGCGCCCTGACCAATGCCCGCTTCCACTTCACCGACATCCGGTCCAGATGC	604
Db	618	AAGCAGTCCGTGCGCTTGACAATGCCAGGATTCATTTTACAGACCAGCGCTTCAGATGC	677
Qy	605	TGCGGAGAGAAGAAGACAGTACTTTCGAGCTGTACGAGGCGCAGCGTGCCCGGTACACGG	664
Db	678	GGAGGAAGAGAAAGACAGTACTTTGACTGTACGAGCAATCTGTGGCTAGGTACATGTG	737
Qy	665	ACCTGCCCGAGAGGCCAACTGA	687
Db	738	ATCTTCTGTGAAAAAGCAAAATTGA	760

RESULT 15

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US-09-376-673-1
; Sequence 1, Application US/09976673
; Patent No. US20020160473A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Fradkov, Arcady
; APPLICANT: Labas, Yulii
; APPLICANT: Matz, Mikhail
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Gurskaya, Nadezda
; TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS
; FILE REFERENCE: CLON-028W0
; CURRENT APPLICATION NUMBER: US/09/976,673
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,018
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60,306,131
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 910
; TYPE: DNA
; ORGANISM: heteractis crispa
US-09-376-673-1

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Query Match 63.3%; Score 435; DB 9; Length 910;
Best Local Similarity 77.3%; Pred. No. 3.9e-102;
Matches 528; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy	5	TTAGCGGCGCTGCTGAGGAGAGTATGCGCATCAAGATGTACATGAGGAGGCACCGTGAACG	64
Db	83	TGCGCTGGTTTGTGTAAGAAAGATATGCGCATCAAGATGTACATGGAAGCAGCGGTTAATG	142
Qy	65	GCACACTACTCAAGTCGGAGGCGGAGGCGACGCGAACCCCTTCGCCGCGACCCAGAGACA	124
Db	143	GCATATATTTCAAGTGTGAGGAGAGGAGACGGCAACCCATTTACAGTATCGCAGAGCA	202
Qy	125	TGAGAATCCAGTCAACGAGGCGCGCCCTTGCCTTCGCTTCGACATCTTGGCGCCCT	184
Db	203	TGAGATTTCATGTACCGAAGGGGCTCCATTACATTTGCTTCGACATTTTGGCACCGT	262
Qy	185	GCTGCGAGTAGCGCAGCAGGACCTTCTGTGCACACACCGCGAGATCCCGGACTTCTTCA	244
Db	263	GTGTGTGATACGGCAGCAGGACCTTGTCCACCATACGGCAGAGATTCGGGATTTCTTCA	322
Qy	245	AGCAGAGCTTCCCGAGGGCTTCACCTGGGAGAGAACCCACCTACGAGGACGGCGCA	304

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|||||
Db 323 AGCAGTCTTTCCCTGAAGGCTTTTACTTTGGAAAGAACCAACCTATGAAGATGGAGGCA 382
QY 305 TCCTGACCGCCACACAGGACACGCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGG 364
Db 383 TTCTTACTGCTCCTCAGGACACAAGCCTGGAGGGGAACCTGCCCTTATATACAAGGTGAAG 442
QY 365 TGCACGGCACCAACTTCCCGCCGACCGGCCCGCTGATGAAGAACAGAGCGCGGCTGGG 424
Db 443 TCCTTGGTACCAATTTTCTGCTGATGGCCCGCTGATGAAGAACAAATCAGGAGGATGGG 502
QY 425 AGCCAGCACGAGTGTGTACCCGAGAACGCGTGTGTGGCGCCGGAACGTGATGG 484
Db 503 AGCCATGCACTGAGGTGTTTATTCAGAGAAATGGTGCTGTGTGGACGTAAATGTGATGG 562
QY 485 CCCTGAAGGTGGCGAACCGGCACCTGATCTGCCACCACTACACAGCTACCGAGCAAGA 544
Db 563 CCCTTAAAGTCGGTGATCGTGGTTTGTATCGCCATCTCTATCTTTACAGGTCCAAGA 622
QY 545 AGGCGTCCGCGCCCTGACCATGCGCGCTTCCACTTCACCGACATCCGGCTCCAGATGC 604
Db 623 AAGCAGTCCGTGCTTGACAAATGCCAGGATTTCAATTTTACAGACATCCGCCCTCAGATGC 682
QY 605 TGGGAGAGAGAGAGACGAGTACTTTCGAGCTGTACGAGGCGCAGCGTGGCCCGGTACAGCG 664
Db 683 CGAGGAAACCGAAGACGAGTACTTTGAACTGTACGAAGCATCTGTGGCTAGGTACAGTG 742
QY 665 ACCTGCCCGAGAGGCCCAACTGA 687
Db 743 ATCTTCTCTGAAAAAGCAAAATTGA 765
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Job time : 605 secs

GenCore version 5.1.6
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(without alignments)
974.426 Million cell updates/sec

Title: US-09-976-673-11

Perfect score: 587
Sequence: 1 atgtgtgagcgcctgtgaa.....tgccggaagggccaactga 687

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Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	687	100.0	687	6	ABL41172 H. crispa
2	671	97.7	687	6	ABL41173 H. crispa
3	671	97.7	1396	6	ABL41174 Cr-449-ta
4	671	97.7	1396	10	ACA61024 DNA encod
5	669.4	97.4	1424	6	ABL41175 Cr-449-ta
6	669.4	97.4	1424	10	ACA61025 DNA encod
7	475	69.1	640	12	ADO56228 Red fluor
8	445.6	65.0	1376	10	ACA61026 DNA encod
9	441.2	64.2	681	6	ABL41170 H. crispa
10	439.6	64.0	681	6	ABL41171 H. crispa
11	438.2	63.8	684	6	ABL41180 H. crispa
12	436.6	63.6	684	6	ABL41169 H. crispa
13	436.6	63.6	760	10	ABA00802 Wild type
14	436.6	63.6	760	10	ABA00806 Multiple
15	435	63.3	910	6	ABL41167 H. crispa
16	435	63.3	910	6	ABL41182 H. crispa
17	431.8	62.9	760	10	ABA00805 Multiple
18	431.8	62.9	760	10	ABA00804 Chromopro
19	431.8	62.9	760	10	ABA00803 Chromopro
20	431.8	62.9	908	6	ABL41168 H. crispa
21	429.2	62.5	680	6	ABL41181 H. crispa

ALIGNMENTS

RESULT 1

ABL41172

ID ABL41172 standard; cDNA; 687 BP.

XX ABL41172;

XX 12-AUG-2002 (first entry)

DE H. crispa fluorescent protein mutant FP10-cr1 encoding cDNA.

XX Stichodactylidae; chromoprotein; fluorescent; anthozoan; food; FRET;
KW colouring agent; pharmaceutical; cosmetic; immunoassay; biosensor; gene;
KW fluorescence resonance energy transfer; gene expression; mutant; ss.
XX Heteractis crispa.
XX Location/Qualifiers
Key 1..687
CDS /*tag= a
/product= "mutant fluorescent protein"

WC200230965-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032080.

XX 12-OCT-2000; 2000US-0240018P.

XX 16-JUL-2001; 2001US-0306131P.

XX (CLON-) CLONTECH LAB INC.

XX Lukanov SA, Pradkov AP, Lukanov KA, Gurskaya NG;

XX WPI; 2002-444170/47.

XX P-PSDB; ABB07994.

PT Novel nucleic acid encoding Stichodactylidae chromoprotein and its
PT fluorescent mutant useful as coloring agent, labels in analyte detection
PT assays, markers in recombinant DNA applications and filters in
PT sunscreens.
XX Claim 5; Fig 10; 81pp; English.

Aaa50885 A. sulcat
Aad46286 Anemonia
Aca61028 DNA encod
Aca61027 DNA encod
Aad46287 Anemonia
Aba00245 C. gigant
Aba00244 C. gigant
Adc24132 Discosoma
Adl46211 Discosoma
Adl46282 Discosoma
Aah47656 Anthozoan
Adc24130 Discosoma
Adl46209 Discosoma
Abz22476 Mammalian
Aad46278 Discosoma
Aad28208 Discosoma
Aad28207 Discosoma
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Adc24128 Discosoma
Adl46207 Discosoma
Adn33980 Mutant-ty
Adc24134 Discosoma
Adl46205 Human cod
Adl46225 Human cod

696 3 AAA50885
707 6 AAD46286
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1404 10 ACA61027
699 6 AAD46287
681 6 ABA00245
835 6 ABA00244
678 11 ADC24132
678 11 ADL46211
678 11 ADL46282
681 4 AAH47656
681 10 ADC24130
681 11 ADL46209
723 8 ABZ22476
678 6 AAD46278
678 6 AAD28208
678 6 AAD28207
695 3 AAA48743
678 10 ADC24128
678 11 ADL46207
704 11 ADN33980
681 10 ADC24134
681 11 ADL46205
681 11 ADL46225

22 422.6 61.5
23 417.8 60.8
24 417.8 60.8
25 415.6 60.5
26 415.2 60.4
27 362.6 52.8
28 361.2 52.6
29 306 44.5
30 306 44.5
31 302.8 44.1
32 298.8 43.5
33 298.2 43.4
34 298.2 43.4
35 297.4 43.3
36 292.4 42.6
37 292.4 42.6
38 292.4 42.6
39 292.4 42.6
40 291.8 42.5
41 291.8 42.5
42 291.8 42.5
43 291.4 42.4
44 291.4 42.4
45 291.4 42.4

CC The invention relates to a nucleic acid present in other than its natural
 CC environment and encoding an Stichodactyliden chromoprotein or its
 CC fluorescent mutant, where the fluorescent protein has an emission maximum
 CC ranging from 580-660 nm. The polynucleotides and encoded proteins are
 CC useful in applications employing a chromo or fluorescent nucleic acid or
 CC protein. Recombinant vectors comprising the nucleic acid is useful for
 CC producing an Anthozoan chromo and/or fluorescent protein. The
 CC chromoproteins, and their fluorescent mutants are useful as colouring
 CC agents capable of imparting colour or pigment to a particular composition
 CC of matter. The chromoproteins can be incorporated into a variety of
 CC different compositions including food compositions, pharmaceuticals,
 CC cosmetics, living organisms, e.g. animals and plants, and as labels in
 CC analyte detection assays, e.g. assays for biological analytes of interest
 CC (see ABL41167 for a detailed description of the various uses of the
 CC chromoproteins). The present sequence represents the H. crispa
 CC fluorescent protein mutant FP10-cr1 encoding cDNA

XX Sequence 687 BP; 150 A; 232 C; 212 G; 93 T; 0 U; 0 Other;

Query Match 100.0%; Score 687; DB 6; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1.3e-111;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGACGGCGCTCTCAAGGAGAGTATGCGCATCAAGATGTACATGATGGAGGACCGTG 60
 DB 1 ATGGTGACGGCGCTCTCAAGGAGAGTATGCGCATCAAGATGTACATGATGGAGGACCGTG 60
 QY 61 AACGCCCACTACTTCAAGTGGAGGGCGAGGGCGCAACCCCTTCGGCGGCCACCCAG 120
 DB 61 AACGCCCACTACTTCAAGTGGAGGGCGAGGGCGCAACCCCTTCGGCGGCCACCCAG 120
 QY 121 AGCATGAGATTCACGTGACCGAGGGCGCCCTTCGCTTCGCTTCGACATCTGGCC 180
 DB 121 AGCATGAGATTCACGTGACCGAGGGCGCCCTTCGCTTCGCTTCGACATCTGGCC 180
 QY 181 CCTCTCTCGAGTACGGCAGCAGACCTTCGTGCACACACCGCGGAGATCCCGACTTC 240
 DB 181 CCTCTCTCGAGTACGGCAGCAGACCTTCGTGCACACACCGCGGAGATCCCGACTTC 240
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 QY 301 GGCATCTCTGACCGCCACAGACACACCGCTGAGGGCACTCCCTGATCTCAAGGTG 360
 DB 301 GGCATCTCTGACCGCCACAGACACACCGCTGAGGGCACTCCCTGATCTCAAGGTG 360
 QY 361 AAGGTGACGGCACCAACTTCCCGCGACCGGCCCTCGTATGAAGAACAGAGCGGCGC 420
 DB 361 AAGGTGACGGCACCAACTTCCCGCGACCGGCCCTCGTATGAAGAACAGAGCGGCGC 420
 QY 421 TGGAGCCGACGACCGAGGTGTGTACCCGAGAACCGCTGCTGTGGCGCGGACGTG 480
 DB 421 TGGAGCCGACGACCGAGGTGTGTACCCGAGAACCGCTGCTGTGGCGCGGACGTG 480
 QY 481 ATGGCCCTTGAAGTGGGCGACCGGCACTGATCTGCACCACTACACAGCTACCGGAGC 540
 DB 481 ATGGCCCTTGAAGTGGGCGACCGGCACTGATCTGCACCACTACACAGCTACCGGAGC 540
 QY 541 AAGAGGCGGTGCGGCGCTGACCATGCGCGCTTCCATTCACCGATCCGCGCTCCAG 600
 DB 541 AAGAGGCGGTGCGGCGCTGACCATGCGCGCTTCCATTCACCGATCCGCGCTCCAG 600
 QY 601 ATGTCGCGGAAGAGAGGAGTACTTTCAGGTGTACAGGCGCAGCGTGGCCCGGTAC 660
 DB 601 ATGTCGCGGAAGAGAGGAGTACTTTCAGGTGTACAGGCGCAGCGTGGCCCGGTAC 660
 QY 661 AGCGACCTGCGCGAGAGGCACTGA 687
 DB 661 AGCGACCTGCGCGAGAGGCACTGA 687

ABL41173
 ID ABL41173 standard; cDNA; 687 BP.
 XX ABL41173;
 AC ABL41173;
 XX 12-AUG-2002 (first entry)
 XX H. crispa alternative fluorescent protein mutant FP10-cr1 cDNA.
 DE Stichodactyliden; chromoprotein; fluorescent; anthozoan; food; FRET;
 XX colouring agent; pharmaceutical; cosmetic; immunoassay; biosensor; gene;
 XX fluorescence resonance energy transfer; gene expression; mutant; ss.
 XX Heteractis crispa.
 OS Location/Qualifiers
 FH 1.687
 CDS /tag= a
 /product= "mutant fluorescent protein"
 FT 4..6
 /tag= b
 /note= "the amino acid Val encoded by the above codon is
 not indicated in the corresponding protein"
 XX WO200230965-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US032080.
 XX 12-OCT-2000; 2000US-0240018P.
 XX 16-JUL-2001; 2001US-0306131P.
 XX (CLON-) CLONTECH LAB INC.
 XX Lukanov SA, Fradkov AF, Lukanov KA, Gurskaya NG;
 WPI: 2002-444170/47.
 DR P-PSDB; ABB07995.
 XX Novel nucleic acid encoding Stichodactyliden chromoprotein and its
 PT fluorescent mutant useful as coloring agent, labels in analyte detection
 PT assays, markers in recombinant DNA applications and filters in
 PT sunscreens.
 XX Claim 5; Fig 10; 81pp; English.
 CC The invention relates to a nucleic acid present in other than its natural
 CC environment and encoding an Stichodactyliden chromoprotein or its
 CC fluorescent mutant, where the fluorescent protein has an emission maximum
 CC ranging from 580-660 nm. The polynucleotides and encoded proteins are
 CC useful in applications employing a chromo or fluorescent nucleic acid or
 CC protein. Recombinant vectors comprising the nucleic acid is useful for
 CC producing an Anthozoan chromo and/or fluorescent protein. The
 CC chromoproteins, and their fluorescent mutants are useful as colouring
 CC agents capable of imparting colour or pigment to a particular composition
 CC of matter. The chromoproteins can be incorporated into a variety of
 CC different compositions including food compositions, pharmaceuticals,
 CC cosmetics, living organisms, e.g. animals and plants, and as labels in
 CC analyte detection assays, e.g. assays for biological analytes of interest
 CC (see ABL41167 for a detailed description of the various uses of the
 CC chromoproteins). The present sequence represents the H. crispa
 CC alternative fluorescent protein mutant FP10-cr1 encoding cDNA
 XX Sequence 687 BP; 145 A; 230 C; 219 G; 93 T; 0 U; 0 Other;
 SQ Query Match 97.7%; Score 671; DB 6; Length 687;
 Best Local Similarity 98.5%; Pred. No. 8e-109;
 Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGTGACGGCGCTCTCAAGGAGAGTATGCGCATCAAGATGTACATGATGGAGGACCGTG 60
 DB 1 ATGGTGACGGCGCTCTCAAGGAGAGTATGCGCATCAAGATGTACATGATGGAGGACCGTG 60

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QY 61 AACGGCCACTTCAAGTCGAGGGCGAGGGCGACGGCAACCCCTTCGCGCGCACCCAG 120
Db 61 AACGGCCACTTCAAGTCGAGGGCGAGGGCGACGGCAACCCCTTCGCGCGCACCCAG 120
QY 121 AGCATGAGAAATCCAGTCACCGAGGGCGGCCCTTCGCTTCGACATCCTCGGC 180
Db 121 AGCATGAGAAATCCAGTCACCGAGGGCGGCCCTTCGCTTCGACATCCTCGGC 180
QY 191 CCCTGCTCGAGTAGCGGAGAGACCTTCGTGACACACCGCGGAGATCCCGACTTC 240
Db 191 CCCTGCTCGAGTAGCGGAGAGACCTTCGTGACACACCGCGGAGATCCCGACTTC 240
QY 241 TTCAGCAGAGCTTCCCGAGGGCTTACCTTGGAGAGAACCCACCTACGAGAGCGC 300
Db 241 TTCAGCAGAGCTTCCCGAGGGCTTACCTTGGAGAGAACCCACCTACGAGAGCGC 300
QY 301 GGCATCTCGACCGCCACCGAGCACACAGCTTCGAGGCACTCCCTGATCTACAAGGTG 360
Db 301 GGCATCTCGACCGCCACCGAGCACACAGCTTCGAGGCACTCCCTGATCTACAAGGTG 360
QY 361 AAGGTGACGGCACCACTTCCCGCGAGCGCCGCTGATGAGAACAGCGCGGC 420
Db 361 AAGGTGACGGCACCACTTCCCGCGAGCGCCGCTGATGAGAACAGCGCGGC 420
QY 421 TGGAGCCCGACCGAGGTGGTGTACCCCGAGAACCGCGTGTGCGCGGAAAGCTG 480
Db 421 TGGAGCCCGACCGAGGTGGTGTACCCCGAGAACCGCGTGTGCGCGGAAAGCTG 480
QY 481 ATGGCCCTGAGGTGGGCGACCGCACTGTCTGCACCACTACACAGCTACCGAGC 540
Db 481 ATGGCCCTGAGGTGGGCGACCGCGGCTGTCTGCCACCACTACACAGCTACCGAGC 540
QY 541 AAGAAGGCGGTGCGCGCCCTCACCATGCCCCGGCTTCCACTTCAACGACATCCGGCTCCAG 600
Db 541 AAGAAGGCGGTGCGCGCCCTCACCATGCCCCGGCTTCCACTTCAACGACATCCGGCTCCAG 600
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Db 601 ATGCTCGGAGAGAGAGAGAGTACTTTCAGCTGTACGAGGCGAGCGTGGCCCGGTAC 660
QY 661 AGGACCTGCGCGAGAGAGGCAACTGA 687
Db 661 AGGACCTGCGCGAGAGAGGCAACTGA 687
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RESULT 3

```
ABL41174
ID ABL41174 standard; DNA; 1396 BP.
XX
AC ABL41174;
XX
DT 12-AUG-2002 (first entry)
DE
DS Cr-449-tandem fusion protein nucleotide sequence.
XX
KW Stichodactylidaen; chromoprotein; fluorescent; anthozoan; food; FRET;
KW colouring agent; pharmaceutical; cosmetic; immunassay; biosensor; gene;
KW fluorescence resonance energy transfer; fusion protein; ds.
XX
OS Synthetic.
OS Heteractis crispa.
XX
FH Key Location/Qualifiers
FT CDS 14..1396
FT /tag= a
FT /product= "Cr-449-tandem fusion protein"
FT misc_feature 698..709
FT /tag= b
FT /note= "linker nucleotide fragment"
XX
PN WO20020965-A2.
XX
```

18-APR-2002.

12-OCT-2001; 2001WO-US032080.

12-OCT-2000; 2000US-0240018P.

16-JUL-2001; 2001US-0306131P.

(CLON-) CLONTECH LAB INC.

Lukyanov SA, Fradkov AP, Lukyanov KA, Gurskaya NG;

WPI; 2002-444170/47.

P-PSDB; ABB07996.

Novel nucleic acid encoding Stichodactylidaen chromoprotein and its
fluorescent mutant useful as coloring agent, labels in analyte detection
assays, markers in recombinant DNA applications and filters in
suncreens.

Disclosure; Fig 12; 81pp; English.

The invention relates to a nucleic acid present in other than its natural
environment and encoding an Stichodactylidaen chromoprotein or its
fluorescent mutant, where the fluorescent protein has an emission maximum
ranging from 580-660 nm. The polynucleotides and encoded proteins are
useful in applications employing a chromo or fluorescent nucleic acid or
protein. Recombinant vectors comprising the nucleic acid is useful for
producing an Anthozoan chromo and/or fluorescent protein. The
chromoproteins, and their fluorescent mutants are useful as colouring
agents capable of imparting colour or pigment to a particular composition
of matter. The chromoproteins can be incorporated into a variety of
different compositions including food compositions, pharmaceuticals,
cosmetics, living organisms, e.g. animals and plants, and as labels in
analyte detection assays, e.g. assays for biological analytes of interest
(see ABL41167 for a detailed description of the various uses of the
chromoproteins). The present sequence represents the H. crispa Cr-449-
tandem fusion protein nucleotide sequence

Sequence 1396 BP; 293 A; 471 C; 444 G; 188 T; 0 U; 0 Other;

Query Match 97.7%; Score 671; DB 6; Length 1396;

Best Local Similarity 98.5%; Pred. No. 7,9e-109;

Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1 ATGGTGAGCGGCTCTGAAGGAGAGTATGCGCATCAAGATATACATGAGGCGCACCGTG 60
Db 710 ATGGTGAGCGGCTCTGAAGGAGAGCATGCGCATCAAGATATACATGAGGCGCACCGTG 769
QY 61 AACGCCACTACTTCAAGTCGAGGGCGAGGGCGAGCAACCCCTTCGCGCGCACCCAG 120
Db 770 AACGCCACTACTTCAAGTCGAGGGCGAGGGCGAGCAACCCCTTCGCGCGCACCCAG 829
QY 121 AGCATGAGAAATCCAGTCACCGAGGGCGGCCCTTCGCTTCGACATCCTCGGC 180
Db 830 AGCATGCGGATCCAGTCACCGAGGGCGGCCCTTCGCTTCGACATCCTCGGC 889
QY 181 CCCTGCTCGAGTAGCGGAGAGACCTTCGTGCAACACCGCGGAGATCCCGACTTC 240
Db 890 CCCTGCTCGAGTAGCGGAGAGACCTTCGTGCAACACCGCGGAGATCCCGACTTC 949
QY 241 TTCAGCAGAGCTTCCCGAGGGCTTACCTTGGAGAGAACCCACCTACGAGAGCGC 300
Db 950 TTCAGCAGAGCTTCCCGAGGGCTTACCTTGGAGAGAACCCACCTACGAGAGCGC 1009
QY 301 GGCATCTCGACCGCCACCGAGCACACAGCTTCGAGGCACTCCCTGATCTACAAGGTG 360
Db 1010 GGCATCTCGACCGCCACCGAGCACACAGCTTCGAGGCACTCCCTGATCTACAAGGTG 1069
QY 361 AAGGTGACGGCACCAACTTCCCGCGAGCGCCCGCTGTAGTGAAGAAAGAGCGCGGC 420
Db 1070 AAGGTGCTGGGACCAACTTCCCGCGAGCGCCCGCTGTAGTGAAGAAAGAGCGCGGC 1129
QY 421 TGGAGCCCGACCGAGGTGGTGTACCCCGAGAACGGCGTGTCTGTGCGCGCGGAAAGCTG 480
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DB 1130 TGGAGCCAGCAGCAGAGTGTGTACCCGAGAACGGCGTGTGTGCGCGCGAGACGTG 1189
 QY 481 ATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCACTACACAGCTACCGGAGC 540
 DB 1190 ATGGCCCTGAAGTGGGCGACCGGCGGTGATCTGCCACCACTACACAGCTACCGGAGC 1249
 QY 541 AAGAGGCGGTGCGCGCCCTGACCATGCGCGGCTTCCACTTCCAGCATCCGGCTCCAG 600
 DB 1250 AAGAGGCGGTGCGCGCCCTGACCATGCGCGGCTTCCACTTCCAGCATCCGGCTCCAG 1309
 QY 601 ATGCTGCGGAGAGAGGAGGAGTACTTCCAGCTGTACGAGGCGCGCGGCTGATC 660
 DB 1310 ATGCTGCGGAGAGGAGGAGGAGTACTTCCAGCTGTACGAGGCGCGCGGCTGATC 1369
 QY 661 AGCGACCTGCCGAGAGGAGGAGGAGTACTTCCAGCTGTACGAGGCGCGCGGCTGATC 687
 DB 1370 AGCGACCTGCCGAGAGGAGGAGGAGTACTTCCAGCTGTACGAGGCGCGCGGCTGATC 1396

RESULT 4
 ID ACA61024 standard; DNA; 1396 BP.
 AC ACA61024;
 XX
 DT 09-JUL-2003 (first entry)
 XX
 DE DNA encoding chromoprotein Cr-449-tandem.
 XX
 KW Chromo/fluorescent domain; labeled fusion protein;
 KW site-specific gene modification; chromoprotein; colouring agent;
 KW food composition; pharmaceutical; cosmetic; Cr-449-tandem; gene; ds.
 XX Anthozoa.

Key Location/Qualifiers
 FH 14..1396
 CDS /*tag= a
 FT /product= "Cr-449-tandem"
 XX

PN WO2003031590-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 10-OCT-2002; 2002WO-US032560.
 XX
 PR 12-OCT-2001; 2001US-00976673.
 PR 11-FEB-2002; 2002US-0356228P.
 PR 22-MAY-2002; 2002US-0383336P.
 XX

PA (CLON-) CLONTECH LAB INC.
 XX

PI Lukyanov SA;
 XX

DR WPI; 2003-381709/36.
 DR P-PSDB; AB009921.
 XX

PT New nucleic acid encoding polypeptide products having at least two linked
 PT chromo/fluorescent domains, useful for generating transgenic plants or
 PT animals or site-specific gene modifications in cell lines.
 XX

PS Disclosure; Fig 1; 68pp; English.
 XX

CC The invention describes a nucleic acid encoding a polypeptide product
 CC comprising a first and a second chromo/fluorescent domain, optionally
 CC joined by a linking domain. The first and second chromo/fluorescent
 CC domains associate with each other under intracellular conditions so that
 CC the encoded polypeptide assumes a tertiary structure. The nucleic acid
 CC and the protein are useful in producing labeled fusion proteins that have
 CC a precise and predictable signal to fusion partner ratio. The nucleic
 CC acid may also be used in generating transgenic, non-human plants or
 CC animals or site-specific gene modifications in cell lines. The

CC Chromoproteins may be used as colouring agents, as a food composition, in
 CC pharmaceuticals or cosmetics, as labels in analyte detection assays or as
 CC selectable markers in recombinant DNA applications. This sequence encodes
 CC chromo/fluorescent domain fusion protein Cr-449-tandem
 XX
 SQ Sequence 1396 BP; 293 A; 471 C; 444 G; 188 T; 0 U; 0 Other;

Query Match 97.7%; Score 671; DB 10; Length 1396;
 Best Local Similarity 98.5%; Pred. No. 7.9e-109;
 Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGTGGAGCGGCTCTCTGAAGGAGAGTATGGCATCAAGATGTATCATGGAGGACCGCTG 60
 DB 710 ATGGTGGAGCGGCTCTCTGAAGGAGAGTATGGCATCAAGATGTATCATGGAGGACCGCTG 769
 QY 61 AACGGCCACTACTTCAAGTGGAGGCGGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 DB 770 AACGGCCACTACTTCAAGTGGAGGCGGAGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 829
 QY 121 AGCATGAGAATCCAGTGCACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
 DB 830 AGCATGCGGATCCAGTGCACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 889
 QY 181 CCCTGCTCGAGTACGGCAGCAGGACCTTCGTGACACACACCGCGGAGATCCCGACTTC 240
 DB 890 CCCTGCTCGAGTACGGCAGCAGGACCTTCGTGACACACACCGCGGAGATCCCGACTTC 949
 QY 241 TTCAGCAGAGCTTCCCGAGGCGGCTTCCCTGGGAGAGAACCCACCTACGAGACGCG 300
 DB 950 TTCAGCAGAGCTTCCCGAGGCGGCTTCCCTGGGAGAGAACCCACCTACGAGACGCG 1009
 QY 301 GGCACTCTGACCGCGCCACCGAGACACCGAGCTTGGAGGCGGCGGCGGCGGCGGCGG 360
 DB 1010 GGCACTCTGACCGCGCCACCGAGACACCGAGCTTGGAGGCGGCGGCGGCGGCGGCGG 1069
 QY 361 AAGGTGACGCGCACCAACTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 DB 1070 AAGGTGCTGGGCGACCAACTTCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1129
 QY 421 TGGGAGCGCGCAGCAGCGAGTGTGTACCCCGAGAACCGCGCTGTGTGCGGCGGCGGCGG 480
 DB 1130 TGGGAGCGCGCAGCAGCGAGTGTGTACCCCGAGAACCGCGCTGTGTGCGGCGGCGGCGG 1189
 QY 481 ATGGCCCTGAAGTGGGCGGACCGGACCTGTATCTGCCACCACTACACAGCTACCGGAGC 540
 DB 1190 ATGGCCCTGAAGTGGGCGGACCGGCGGCTGTATCTGCCACCACTACACAGCTACCGGAGC 1249
 QY 541 AAGAGGCGGTGCGCGCCCTGACCATGCGCGGCTTCCACTTCCAGCATCCGGCTCCAG 600
 DB 1250 AAGAGGCGGTGCGCGCCCTGACCATGCGCGGCTTCCACTTCCAGCATCCGGCTCCAG 1309
 QY 601 ATGCTGCGGAGAGAGAGGAGGAGTACTTCCAGCTGTGTACGAGGCGCGGCTGATC 660
 DB 1310 ATGCTGCGGAGAGAGGAGGAGGAGTACTTCCAGCTGTGTACGAGGCGCGGCTGATC 1369
 QY 661 AGCGACCTGCCGAGAGGAGGAGGAGTACTTCCAGCTGTGTACGAGGCGCGGCTGATC 687
 DB 1370 AGCGACCTGCCGAGAGGAGGAGGAGTACTTCCAGCTGTGTACGAGGCGCGGCTGATC 1396

RESULT 5
 ID ABL41175 standard; DNA; 1424 BP.
 XX
 AC ABL41175;
 XX
 DT 12-AUG-2002 (first entry)
 XX

DE Cr-449-tandem-actin fusion protein nucleotide sequence.
 XX

XX Stichodactylidae; chromoprotein; fluorescent; anthozoan; food; FRET;
 KW colouring agent; pharmaceutical; cosmetic; immunoassay; biosensor; gene;
 KW fluorescence resonance energy transfer; fusion protein; ds.


```

XX OS Synthetic.
XX OS Heteractis crispa.
XX FH Location/Qualifiers
XX FT 14. .1423
XX FT /*tag= a
XX FT /product= "Cr-449-tandem-actin fusion protein"
XX FT /note= "the stop codon is not indicated"
XX FT 598. .709
XX FT misc_feature
XX FT /*tag= b
XX FT /note= "linker nucleotide fragment"
XX FT 1394. .1405
XX FT /*tag= c
XX FT 1406. .1423
XX FT /*tag= d
XX FT /note= "partial actin fragment"
XX XX
XX PN WO200230965-A2.
XX PN
XX PD 18-APR-2002.
XX XX
XX PF 12-OCT-2001; 2001WO-US032080.
XX XX
XX PF 12-OCT-2000; 2000US-0240018P.
XX PR 16-JUL-2001; 2001US-0306131P.
XX XX
XX PA (CLON-) CLONTECH LAB INC.
XX XX
XX PI Lukyanov SA, Fradkov AF, Lukyanov KA, Gurskaya NG;
XX XX
XX DR WPI; 2002-444170/47.
XX DR P-PSDB; ABB07997.
XX XX
XX PT Novel nucleic acid encoding Stichodactyliden chromoprotein and its
XX PT fluorescent mutant useful as coloring agent, labels in analyze detection
XX PT assays, markers in recombinant DNA applications and filters in
XX PT sunscreens.
XX PS
XX PS Disclosure; Fig 13; 81pp; English.
XX XX
XX CC The invention relates to a nucleic acid present in other than its natural
XX CC environment and encoding an Stichodactyliden chromoprotein or its
XX CC fluorescent mutant, where the fluorescent protein has an emission maximum
XX CC ranging from 580-660 nm. The polynucleotides and encoded proteins are
XX CC useful in applications employing a chromo or fluorescent nucleic acid or
XX CC protein. Recombinant vectors comprising the nucleic acid is useful for
XX CC producing an Anthozoan chromo and/or fluorescent protein. The
XX CC chromoproteins, and their fluorescent mutants are useful as colouring
XX CC agents capable of imparting colour or pigment to a particular composition
XX CC of matter. The chromoproteins can be incorporated into a variety of
XX CC different compositions including food compositions, pharmaceuticals,
XX CC cosmetics, living organisms, e.g. animals and plants, and as labels in
XX CC analyte detection assays, e.g. assays for biological analyses of interest
XX CC (see ABU41167 for a detailed description of the various uses of the
XX CC chromoproteins). The present sequence represents the H. crispa Cr-449-
XX CC tandem-actin fusion protein nucleotide sequence
XX XX
XX SQ Sequence 1424 BP; 301 A; 477 C; 452 G; 194 T; 0 U; 0 Other;
XX XX
XX Query Match 97.4%; Score 669.4; DB 6; Length 1424;
XX Best Local Similarity 98.4%; Pred. No. 1.5e-108;
XX Matches 676; Conservative 0; Mismatches 11; Indels 0; Gaps 0
XX XX
QY 1 ATGGTGAGCGGCTCTGAAGGAGAGTAGTCGCATCAAGATGTACATGAGGGCACCGTG 60
XX
Db 14 ATGGTGAGCGGCTCTGAAGGAGAGTAGTCGCATCAAGATGTACATGAGGGCACCGTG 73
XX
QY 61 AACGGCCACTACTTCAAGTCGGGGGCGAGCGGCAACCCCTTCGCGGCAACCG 120
XX
Db 74 AACGGCCACTACTTCAAGTCGGGGGCGAGCGGCAACCCCTTCGCGGCAACCG 133
XX
QY 121 AGCATGAGAATCCAGTCGACCGAGGGGGCCCCCTCGCCCTTCGCCCTTCGACATCTCGGC 180

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XX PA (CLON-) CLONTECH LAB INC.
XX PI Lukanov SA;
XX DR WPI; 2003-381709/36.
XX DR P-PSDB; AB009922.
XX PT New nucleic acid encoding polypeptide products having at least two linked
XX PT chromo/fluorescent domains, useful for generating transgenic plants or
XX PT animals or site-specific gene modifications in cell lines.
XX PS Disclosure; Fig 2; 68pp; English.
XX
XX The invention describes a nucleic acid encoding a polypeptide product
XX comprising a first and a second chromo/fluorescent domain, optionally
XX joined by a linking domain. The first and second chromo/fluorescent
XX domains associate with each other under intracellular conditions so that
XX the encoded polypeptide assumes a tertiary structure. The nucleic acid
XX and the protein are useful in producing labeled fusion proteins that have
XX a precise and predictable signal to fusion partner ratio. The nucleic
XX acid may also be used in generating transgenic, non-human plants or
XX animals or site-specific gene modifications in cell lines. The
XX chromoproteins may be used as colouring agents, as a food composition, in
XX pharmaceuticals or cosmetics, as labels in analyte detection assays or as
XX selectable markers in recombinant DNA applications. This sequence encodes
XX chromo/fluorescent domain fusion protein Cr-449-tandem-actin
XX
XX Sequence 1424 BP; 301 A; 477 C; 452 G; 194 T; 0 U; 0 Other;
Query Match 97.4%; Score 669.4; DB 10; Length 1424;
Best Local Similarity 98.4%; Pred. No. 1.5e-108;
Matches 676; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 1 ATGTGAGCGGCTCTGAAGAGAGATGTCGATCAAGATGTTACATGGAGGACCGTG 60
DB 14 ATGTGAGCGGCTCTGAAGAGAGATGTCGATCAAGATGTTACATGGAGGACCGTG 73
QY 61 AACGCCCACTTCAAGTGGAGGCGGAGGCGGACCGACCCCTTCGGCGGACCCAG 120
DB 74 AACGCCCACTTCAAGTGGAGGCGGAGGCGGACCGACCCCTTCGGCGGACCCAG 133
QY 121 AGCATGAGATCCACGTGACCGAGGCGGCGCCCTTCGCTTCGACATCCTGGCC 180
DB 134 AGCATGCGGATCCACGTGACCGAGGCGGCGCCCTTCGCTTCGACATCCTGGCC 193
QY 181 CCCTGCTGGAGTACGGAGGAGGACCTTCGTCGACACACCGCGGAGATCCCGGATTC 240
DB 194 CCCTGCTGGAGTACGGAGGAGGACCTTCGTCGACACACCGCGGAGATCCCGGATTC 253
QY 241 TTCAGCAGAGGCTTCCCGAGGGTTCACCTGGGAGAGAACACCACTACGAGGAGCGG 300
DB 254 TTCAGCAGAGGCTTCCCGAGGGTTCACCTGGGAGAGAACACCACTACGAGGAGCGG 313
QY 301 GCATCTCTGACCGCCACAGACACGAGCTGAGGGCACTGCTGATCTACAGGTG 360
DB 314 GCATCTCTGACCGCCACAGACACGAGCTGAGGGCACTGCTGATCTACAGGTG 373
QY 361 AAGGTGACCGGACCACTTCCCGCCGACGCGCCGCTGATGAAGAACAGAGCGGCGGC 420
DB 374 AAGGTGCTGGGACCACTTCCCGCCGACGCGCCGCTGATGAAGAACAGAGCGGCGGC 433
QY 421 TGGAGCCACAGACCGAGGTGTTGATCCCGGAGAACGCGCTGCTGCGGCGGAGCGTG 480
DB 434 TGGAGCCACAGACCGAGGTGTTGATCCCGGAGAACGCGCTGCTGCGGCGGAGCGTG 493
QY 481 ATGGCCCTGAAGGTGGGCGACCGGACCTGATCTGCCACCACTACACGAGTCCCGGAGC 540
DB 494 ATGGCCCTGAAGGTGGGCGACCGGCGGCTGATCTGCCACCACTACACGAGTCCCGGAGC 553
QY 541 AAGAGGCGGTGCGGCGCCTGACCATGCGCGGTTCACCTTCACCGACATCCGCGTCCAG 600
DB 554 AAGAGGCGGTGCGGCGCCTGACCATGCGCGGTTCACCTTCACCGACATCCGCGTCCAG 613

QY 601 ATGCTGCGGAGAGAGAGGACGAGTACTTCGAGCTGTACGAGGCGGCGGCTAC 660
DB 614 ATGCTGCGGAGAGAGAGGACGAGTACTTCGAGCTGTACGAGGCGGCGGCTAC 673
QY 661 ACGGACCTGCGGAGAGAGGCGGCAACTGA 687
DB 674 ACGGACCTGCGGAGAGAGGCGGCAACTGA 700
RESULT 7
AD056228
ID AD056228 standard; DNA; 640 BP.
XX AC AD056228;
XX AC AD056228;
XX DT 26-AUG-2004 (first entry)
XX DE Red fluorescent chromoprotein rGFP polynucleotide.
XX KW RNA splicing; RNA processing; gene silencing; disease prevention;
XX KW disease treatment; SPINAI; splicing-component intron;
XX KW red fluorescent chromoprotein; rGFP; ds.
XX OS Synthetic.
XX PN US2004106566-A1.
XX PD 03-JUN-2004.
XX PF 15-MAY-2003; 2003US-00439262.
XX PR 17-MAY-2002; 2002US-0381651P.
XX PR 16-SEP-2002; 2002US-0411062P.
XX PR 12-OCT-2002; 2002US-0418403P.
XX PA (LINS/) LIN S.
XX PA (YING/) YING S.
XX PI Lin S, Ying S;
XX XX WPI; 2004-419483/39.
DR Inducing RNA splicing/processing-associated gene silencing effects, by
PT constructing recombinant nucleic acid composition, cloning composition
PT into vector, introducing vector into cell, generating RNA transcript of
PT composition.
PS Example 3; SEQ ID NO 12; 33pp; English.
XX The invention describes a method of inducing (M1) RNA splicing/processing
XX -associated gene silencing effects. The method involves: constructing a
XX recombinant nucleic acid composition (I) containing an intron (II)
XX flanked with several exons, where (II) can be cleaved out of the exons by
XX RNA splicing and/or processing for gene silencing, and the exons can be
XX linked together to form a gene with desired function; cloning (I) into an
XX expression-competent vector; introducing the vector into a cell; cells,
XX tissue or in vivo; generating RNA transcript of (I); and releasing the
XX metabolic products of (II) by RNA splicing/processing mechanisms, so as
XX to provide gene silencing effects against the genes containing sequences
XX homologous to (II). (M1) is useful for inducing RNA splicing/processing-
XX associated gene silencing effects and in disease prevention and
XX treatment. This sequence represents a red fluorescent chromoprotein rGFP
XX polynucleotide from which the exons are generated for the creation of an
XX artificial gene for examining the RNA splicing/processing-associated gene/
XX silencing effects.
SQ Sequence 640 BP; 140 A; 212 C; 199 G; 89 T; 0 U; 0 Other;
Query Match 69.1%; Score 475; DB 12; Length 640;
Best Local Similarity 92.5%; Pred. No. 1.9e-74;
Matches 637; Conservative 0; Mismatches 0; Indels 52; Gaps 11;

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QY 1 ATGGTGAGCGGCTCTCTGAAGGAGAGTATGCGCATCAAGATGTACATGAGGCGCACCGTG 60
Db 1 ATGGTGAGCGGCTCTCTGAAGGAGAGTATGCGCATCAAGATGTACATGAGGCGCACCGTG 60
QY 61 AACGGCCACTACTTCAAGTGCAGGCGGAGGCGGAGGCGAACCCCTTCGCCGGCACCCAG 120
Db 61 AACGGCCACTACTTCAAGTGCAGGCGGAGGCGGAGGCGAACCCCTTCGCCGGCACCCAG 119
QY 121 AGCATGAGAAATCCAGTGAACCGAGGCGCCCGCTTCGCCCTTCGACATCTGTGGC 180
Db 120 AGCATGAGAAATCCAGTGAACCGAGGCGCCCGCTTCGCCCTTCGACATCTGTGG-C 178
QY 181 CCTGCTCGAGTAGGAGGAGAG---GACCTTCGTGACACACCGCGCGAGATCCCGAC 237
Db 179 CCTGCTCGAGTAGGAGGAGAGAGCTTCGTGACACACCGCGCGAGATCCCGGAG- 237
QY 238 TTCTTTCAAGCAGAGCTTCCCGAGGGCTTCACTCGGAGAGAAACCAACCATCAGGAG 297
Db 238 TTCTTTCAAGCAGAGCTTCCCGAGGGCTTCACTCGGAG----- 276
QY 298 GCGGCACTCTGACCGCCACAGGACACAGACTCTGGAGGGCACTGCTGTATCTACAAG 357
Db 277 -----ACCAGGACACCAAGCTTGGAG-GGCAACTGCTGTATCTACAAG 316
QY 358 GTGAAGGTGCAGCGCAACAACTTCCCGCGAGCGCCCGGTGATGAAGAACAAAGAGCGC 417
Db 317 GTGAAGGTGCAGCGCAACAACTTCCCGCGAGCGCCCGGTGATGAAGAACAAAGAGCGC 375
QY 418 GCTGGAGCGCCAGCACCGAGTGTGTACCCCGAGAACGCGTGTCTGTGCGCGCGAAG 477
Db 376 GCTGGAGCGCCAGCACCGAGTGTGTACCCCGAGAAC-GCGTGTCTGTGCGCGCGAAG 434
QY 478 GTGATGGCCCTGAAGTGGGCGGACCGGACCTGTCTGACCACTACACAGTACCGG 537
Db 435 GTGATGGCCCTGAAGTGGGCGGACCGGACCTGTCTG-CACCACTACACAGTACCGG 493
QY 538 AGCAAGAGCGCGTGGCGCCCTGACCATGCGCGCTTCCACTTCACCGACATCCGGCTC 597
Db 494 AGCAAGAGCGCGTGGCGCCCTGACCATGCGCGCTT-CACCTTCACCGACATCCGGCTC 552
QY 598 CAGATGCTCGGAGAAAGAGACGAGTACTTTCAGCTGTACGAGGCGGAGCGTGGCGCG 657
Db 553 CAGATGCTCGGAGAAAGAGACGAGTACTTTCAGCTGT-ACGAGGCGGAGCGTGGCGCG 611
QY 658 TACAGCGACCTGCGCGGAGAGGCGCAACTG 686
Db 612 TACAGCGACCTGCGCGGAGAGGCGCAACTG 640
```

RESULT 8

ACA61026

ID ACA61026

XX

AC ACA61026;

XX

DT 09-JUL-2003 (first entry)

XX

DE DNA encoding chromoprotein HcRed-Crl-tandem.

XX

KW Chromo/fluorescent domain; labeled fusion protein;

KW site-specific gene modification; chromoprotein; colouring agent;

KW food composition; pharmaceutical; cosmetic; HcRed-Crl-tandem; gene; ds.

XX

OS Anthozoa.

XX

FH Key

FT 1. 1376

FT CDS

FT /tag= a

FT /product= "HcRed-Crl-tandem"

FT /trans_except= (pos:679..680, aa:Asn)

XX

PN WO2003031590-A2.

XX

PD 17-APR-2003.

XX

PF 10-OCT-2002; 2002WO-US032560.

XX

PR 12-OCT-2001; 2001US-00976673.

XX

PR 11-FEB-2002; 2002US-0356225P.

XX

PR 22-MAY-2002; 2002US-0383336P.

XX

PA (CLON-) CLONTECH LAB INC.

XX

XX Lukyanov SA;

XX

XX WPI; 2003-381709/36.

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XX P-PSDB; ABU09923.

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XX OS Heteractis crispa.
 XX PH Key Location/Qualifiers
 XX FT 1..681
 XX FT /*tag= a
 XX FT /product= "mutant fluorescent protein"
 XX FN WO200230965-A2.
 XX PD 18-APR-2002.
 XX PF 12-OCT-2001; 2001WO-US032080.
 XX XX 12-OCT-2000; 2000US-0240018P.
 XX PR 16-JUL-2001; 2001US-0306131P.
 XX XX (CLON-) CLONTECH LAB INC.
 XX PI Lukyanov SA, Fradkov AP, Lukyanov KA, Gurskaya NG;
 XX DR WPI; 2002-444170/47.
 XX DR P-PSDB; ABB07993.
 XX PT Novel nucleic acid encoding Stichodactyliden chromoprotein and its
 XX PT fluorescent mutant useful as coloring agent, labels in analyte detection
 XX PT assays, markers in recombinant DNA applications and filters in
 XX PT sunscreens.
 XX PS Claim 5; Fig 8; 81pp; English.

The invention relates to a nucleic acid present in other than its natural environment and encoding an Stichodactyliden chromoprotein or its fluorescent mutant, where the fluorescent protein has an emission maximum ranging from 580-660 nm. The polynucleotides and encoded proteins are useful in applications employing a chromo or fluorescent nucleic acid or protein. Recombinant vectors comprising the nucleic acid is useful for producing an Anthozoan chromo and/or fluorescent protein. The chromoproteins, and their fluorescent mutants are useful as coloring agents capable of imparting colour or pigment to a particular composition of matter. The chromoproteins can be incorporated into a variety of different compositions including food compositions, pharmaceuticals, cosmetics, living organisms, e.g. animals and plants, and as labels in analyte detection assays, e.g. assays for biological analytes of interest (see ABL41167 for a detailed description of the various uses of the chromoproteins). The present sequence represents the H. crispa fluorescent protein mutant 44-6 encoding cDNA

SQ Sequence 681 BP; 185 A; 145 C; 178 G; 173 T; 0 U; 0 Other;

Query Match 64.0%; Score 439.6; DB 6; Length 681;
 Best Local Similarity 78.0%; Pred. No. 3e-68;
 Matches 529; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 10 GGCCTGCTGAGGAGATGATCGCATCAAGTGTACATGTGAGGCGCACCGTGAACGGCCAC 69
 DB 4 GGTGTGTTGAAGAAGATGCGCATCAAGATGTACATGGAAGCGCGTAAATGGCCAT 63
 QY 70 TACTTCAAGTCGAGGGCGAGCGGACCGCAACCCCTTCGCCGCACCCAGAGCATGAGA 129
 DB 64 TATTCAAGTGTGAAGGAGAGGAGACGGACACCCATTTCAGTACGAGAGCATGAGG 123
 QY 130 ATCCACGTGACCGAGGGGCGCCCTTCGCTTCGCTTCGACATCCTGGGCCCTGTGTC 189
 DB 124 ATTCATGTCCAGGAGGGGCTCCATTACCATTTGCTTCGACATTTTGGCACCGTGTGT 183
 QY 190 GAGTACGGCAGCAGACCTTCGTGCACACACCGCGAGATCCCGCACTTCTTCAACGAG 249
 DB 184 CGGTACGGCAGCAGACCTTTGTCCACCATACGAGAGATTCGCCATTTCCTTCAACGAG 243
 QY 250 AGCTTCCCGGCGCTTCACCTGGGAGAGAACCCACCTACGAGGACGGCGCATCTTG 309
 DB 244 TCTTTCCTGGAAGGCTTTACTTTGGGAAGAACCAACCTATGAATGAGGAGCATCTT 303

QY 310 ACCGCCACCAGGACACAGCCTCGAGGGCAACTGCTGATCTACAAGTGAAGTGCAC 369
 DB 304 ACTGCTCATCAGACACAGCCTCGAGGGAACTGCTTATATACAAGTGAAGTCTTT 363
 QY 370 GGCACCACTTCCCGCCGACCGCCCGTGTATGAGAACAGAGCGCGGCTGGAGGCC 429
 DB 364 GGTACCAATTTTCCCTGCTGATGGCCCGGTGATGAAGAACAAATCAGGAGGATGGAGCCA 423
 QY 430 AGCACCGAGGTGTGTACCCCGAGAACCGCGTGTGTGCGCGCGAAAGTGTATGCGCCCTG 489
 DB 424 AGCACTGAGTGTGTTATCCAGAGAAATGGTGTCTGTGTGGACGTAATGTATGCGCCCTT 483
 QY 490 AAGTGGGCGACCGGACCTGTATCTGCACACACTACACAGCTACCGAGACAGAGGCC 549
 DB 484 AAAGTCGGTGTGTCGTGTTGATCTGCCATCACTACTTCTTACAGSTCCCAAGAAGCA 543
 QY 550 GTGCGCGCCCTGACCATGCCCGCTTCACATTCACCGACATCCGGCTCCAGATGCTGGG 609
 DB 544 GTCCGTGCTTGACAAATGCCAGANTTCATTTTACAGACATCCGCTTCAGATGCTGAGG 603
 QY 610 AAGAAGAGGAGGAGTACTTCCAGTGTACGAGGCGGCGTGGCCCGGTACAGCACTG 669
 DB 604 AAGAGAAAGACGAGTACTTTGAAGTGTACGAAGCATCTGTGGTAGGTACAGTGTATCT 663
 QY 670 CCGGAGAGGCCCAACTGA 687
 DB 664 CTTGAAAGACAAATTGA 681

RESULT 11

ABL41180

ID ABL41180 standard; cDNA; 684 BP.

XX ABL41180;

XX 12-AUG-2002 (first entry)

XX H. crispa chromoprotein mutant hcCP mut C148S encoding cDNA.
 XX Stichodactyliden; chromoprotein; fluorescent; anthozoan; food; FRET;
 XX colouring agent; pharmaceutical; cosmetic; immunoassay; biosensor; gene;
 XX fluorescence resonance energy transfer; gene expression; mutant; ss.
 XX Heteractis crispa.

XX Key Location/Qualifiers
 XX CDS 1..684
 XX /*tag= a
 XX /product= "mutant fluorescent protein"

WO200230965-A2.

18-APR-2002.

12-OCT-2001; 2001WO-US032080.

12-OCT-2000; 2000US-0240018P.

16-JUL-2001; 2001US-0306131P.

(CLON-) CLONTECH LAB INC.

Lukyanov SA, Fradkov AP, Lukyanov KA, Gurskaya NG;

WPI; 2002-444170/47.

P-PSDB; ABB07998.

XX Novel nucleic acid encoding Stichodactyliden chromoprotein and its
 XX fluorescent mutant useful as coloring agent, labels in analyte detection
 XX assays, markers in recombinant DNA applications and filters in
 XX sunscreens.
 XX Example; Fig 15; 81pp; English.

Db 62 GCCATTATTTCAAGTGTGAAGGAGGAGGAGCGCAACCCATTTACAGGTACGAGCA 121
QY 125 TGAGAAATCCAGTGAACGAGGCGCCCTGCTGCTTGCCTTCGACATCCTGGCCCTT 184
Db 122 TGAGGATTCATGTACCGAAGGGGCTCCATTTACCATTTGCTTCGACATTTGGCACCGT 181
QY 185 GCTCGAGTACGGCAGCAGGACCTTCTGTGACACACCGCGGAGATCCCGACTTCTTCA 244
Db 182 GTTGTGAGTACGGCAGCAGGACCTTCTGTGACACACCGCGGAGATCCCGACTTCTTCA 241
QY 245 AGCAGAGCTTCCCGAGGCTTCACTTGGGAGAGAACACACCTACGAGGACGGGGCA 304
Db 242 AGCAGTCTTTCCTCGAAGGCTTTACTTGGGAAAGAACACACCTATGAAGATCGAGGCA 301
QY 305 TCCTGACGCGCCACAGACACACGCTGAGGGCACTGCTGATCTCAAGGTGAAG 364
Db 302 TTCTTACTGCTCATAGACACAAAGCTTGGAGGGAATGCTTATATATCAAGGTGAAG 361
QY 365 TGCACGCGACCAACTTCCCGCGACGCGCCCGTGTGATGAAGAACAGGCGGCTGGG 424
Db 362 TCCTTGGTACCAATTTCTGCTGATGGCCCGGTGATGAAGAACAAATCAGGAGGATGG 421
QY 425 AGCCGACGACGAGGTGTACCCGAGAACGCGCTGCTGCGGCGCGAAGCTGATGG 484
Db 422 AGCAAGCAGTGTGCTTATCCAGAGATGCTGCTGCTGTGGACGTAATGTGATGG 481
QY 485 CCCTGAAGGTGGCGACCGGACCTGATCTGCCACCACTACACAGCTACCGGACGAAGA 544
Db 482 CCCTTAAGTCGGTGATCGTGGTTGATCTGCCATCTCTATCTTTCAGGTCCAAGA 541
QY 545 AGGCGGTGCGCGCTGACCATGCGCGCTTCCACTTACCGACATCCGCGTCCAGATGC 604
Db 542 AAGCAGTCCGTCCTTGACATGCGCAGGATTTCAATTTACAGACATCCGCTTCAGATGC 601
QY 605 TCGGAGAGAGAGACGAGTACTTCCAGCTGTACGAGGCGAGCGTGGCCCGGTACAGCG 664
Db 602 CGAGAGAAACGAGAGAGTACTTTGACTGTACGAGCATCTGTGGCTAGGTACATG 661
QY 665 ACCTGCGCGAGAGCGCAACTGA 687
Db 662 ATCTTCTCTGMAAAGCAAAITGA 684

RESULT 13

ABA00802
ID ABA00802 standard; cDNA; 760 BP.

XX AC ABA00802;

XX DT 01-APR-2003 (first entry)

XX DE Wild type chromoprotein cDNA.

XX KW Gene; kindling fluorescent protein; kindling stimulus; movement;
KW labeling; fluorescence resonance energy transfer; FRET;
KW bioluminescence resonance energy transfer; BRET; biosensor;
KW automated screening; ss.

XX OS Heteractis crisp.

XX FH Key Location/Qualifiers

XX FT CDS

XX FT 77..760
XX FT /*tag= a
XX FT /product= "Chromoprotein"

XX XX WO200296924-A1.

XX XX 05-DEC-2002.

XX XX 24-MAY-2002; 2002WO-US016379.

XX XX 25-MAY-2001; 2001US-0293752P.

XX XX 11-OCT-2001; 2001US-0329176P.

XX PA

(CLON-) CLONTECH LAB INC.

XX PI Lukyanov SA, Chudakov D, Lukyanov K;

XX DR WPI; 2003-156788/15.

XX DR P-PSDB; AAG79765.

XX PT Novel nucleic acid that is present in other than its natural environment
XX PT and that encodes kindling fluorescent protein, is useful in labeling
XX PT protocols, e.g. labeling proteins, organelles, cells and organisms.

XX PS Example; Fig 4; 96pp; English.

XX CC The sequences given in ABA00799-805 encode wild type and mutant kindling
XX CC fluorescent proteins. The proteins go from a first substantially non-
XX CC fluorescent or non-fluorescent state to a second fluorescent state upon
XX CC exposure to a kindling stimulus. The kindling proteins are useful for
XX CC detecting an entity such as a protein, organelle or cell in a composition
XX CC such as a cell or a multicellular composition (preferably a multicellular
XX CC organism), by providing the entity as an entity labeled with the kindling
XX CC protein, kindling the kindling fluorescent protein label with a kindling
XX CC stimulus to produce a kindling fluorescent protein label, and
XX CC exciting the kindling fluorescent protein label with light and
XX CC detecting any fluorescence from it to detect the entity. The method
XX CC monitors the movement of the entity. The fluorescent proteins and the
XX CC cDNA encoding them are useful in labeling protocols, e.g., labeling
XX CC proteins, organelles, cells and organisms, as biological labels or
XX CC markers, in protein labeling or tagging applications. The fluorescent
XX CC kindling proteins are useful as detectable labels, as labels in analyte
XX CC detection assays, in fluorescence resonance energy transfer (FRET)
XX CC applications, in bioluminescence resonance energy transfer (BRET)
XX CC applications, as biosensors in prokaryotic and eukaryotic cells, in
XX CC applications involving the automated screening of arrays of cells
XX CC expressing fluorescent reporting groups, in high through-put screening
XX CC assays, as second messenger detectors, and in fluorescent activated cell
XX CC sorting assays

XX SQ Sequence 760 BP; 209 A; 166 C; 189 G; 196 T; 0 U; 0 Other;

Query Match 63.6%; Score 436.6; DB 10; Length 760;

Best Local Similarity 77.5%; Pred. No. 1e-67;

Matches 529; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 5 TGAGCGGCTGCTGAAGGAGAGTATGCGCATCAAGATCTACTAGAGGCGACCGTGAACG 64
Db 78 TGGCTGGTTTGTGAAGAAAGTATGCGCATCAAGATCTACTAGAGGCGACCGTGAATG 137
QY 65 GCACACTACTTTCAAGTGCAGGCGGCGAGCGCAACCCCTTCGCCGCGACCCAGAGCA 124
Db 138 GCATTAATTTCAAGTGTGAGGAGGAGAGCGGCAACCCATTTACAGGTACGAGAGCA 197
QY 125 TGAGAAATCCAGTGAACGAGGCGCGCCCTGCTGCTTCCGCTTCGACATCTCGGCCCT 184
Db 198 TGAGGATTTCATGTCACCGAAGGGGTCCATTACCAATTTGCCTTCGACATTTTGGACCGT 257
QY 185 GCTCGAGTACGCGCAGCAGGACCTTCGTGCGACCAACCGCGAGATCCCGACTTCTTCA 244
Db 258 GTTGTGAGTACGCGCAGGACCTTTGTCACCATACGCGCAGAGATTCGCGATTTCTTCA 317
QY 245 AGCAGAGCTTCCCGAGGGCTTTCACCTGGGAGAGAACCCACCTTACGAGGACGCGGCA 304
Db 318 AGCAGTCTTTCCCTGAAGGCTTTACTTGGAAAGAAACCAACCACTATGAAGATGAGGCA 377
QY 305 TCTGACCGCCACGAGACACCGCTGAGGGCACTGCTGATGATCTACAGGTGAAG 364
Db 378 TTTCTTACTGCTCATCAGGACACAGCCTGGAGGGAACTGCGCTTATATACAGGTGAAG 437
QY 365 TGCACGCGCAACAACTTCCCGCGCGCGCTGATGAAGAACAAAGACGCGCGCTGGG 424
Db 438 TCTTGTGTACCAATTTTCTGCTGTGATGCGCCGCTGATGAGAACAAATCAGGAGATGG 497
QY 425 AGCCGACGACCGAGGTGTGTACCCCGAGAACGCGGTCTGTGCGCGCGGACGATGG 484

Db 498 AGCCATGACACGAGTGGTTTATCCAGAGAATGGTCTCTGTGGACGTAATGTGATGG 557
Qy 485 CCCTGAAGTGGCGGACCGGACCTGATCTGCCACCACTACACCAGCTACCGGAGCAAGA 544
Db 558 CCCTTAAAGTCGGTGATGCTGCTTGAATCTGCCATCTCTATCTCTTACAGTCCAGA 617
Qy 545 AGGCGGTGCGGCGCCCTGACCATGCGCGCTTCCACTTCAACGACATCCGGCTCCAGATGC 604
Db 618 AAGCAGTCCGTGCTGACATGCGGATTCATTTCAGACATCCGCTTCAGATGC 677
Qy 605 TCGCGAAGAAAGGACGAGTACTTCAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCG 664
Db 678 CGAGGAAAGAAAGACGAGTACTTGAACGTGTACGAGCATCTGTGGCTAGGTACAGTG 737
Qy 665 ACCTGCCCGAGAGGCCCAACTGA 687
Db 738 ATCTCTCTGAAAGACCAATTGA 760

RESULT 14

ID ABA00806

XX ABA00806 standard; cDNA; 760 BP.

AC ABA00806;

XX 01-APR-2003 (first entry)

XX Multiple mutant Chromoprotein #2 cDNA.

XX Gene; kindling fluorescent protein; kindling stimulus; movement;

KW labeling; fluorescence resonance energy transfer; FRET;

KW bioluminescence resonance energy transfer; BRET; biosensor;

KW automated screening; ss.

XX Heteractis crispa.

XX Key Location/Qualifiers

PH 77..760

FT /*tag= a

FT /product= "Multiple mutant Chromoprotein #2"

FT replace(182,A)

FT /*tag= c

FT replace(503,T)

FT /*tag= m

FT replace(549..550, AT)

FT /*tag= n

FT replace(594,T)

FT /*tag= h

FT replace(662..663, AT)

FT /*tag= j

FT replace(678,C)

FT /*tag= o

FT replace(686,A)

FT /*tag= i

XX WO200296924-A1.

PN PD

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-US016379.

XX 25-MAY-2001; 2001US-0293752P.

PR 11-OCT-2001; 2001US-0329176P.

XX (CLON-) CLONTECH LAB INC.

XX Lukyanov SA, Chudakov D, Lukyanov K;

XX WPI; 2003-156788/15.

DR P-PSDB; AAG79769.

XX Novel nucleic acid that is present in other than its natural environment

PT and that encodes kindling fluorescent protein, is useful in labeling
PT protocols, e.g. labeling proteins, organelles, cells and organisms.
XX
PS Example; Fig 8; 96pp; English.

XX The sequences given in ABA00799-805 encode wild type and mutant kindling
CC fluorescent proteins. The proteins go from a first substantially non-
CC fluorescent or non-fluorescent state to a second fluorescent state upon
CC exposure to a kindling stimulus. The kindling proteins are useful for
CC detecting an entity such as a protein, organelle or cell in a composition
CC such as a cell or a multicellular composition (preferably a multicellular
CC organism), by providing the entity as an entity labeled with the kindling
CC protein, kindling the entity as an entity labeled with a kindling
CC stimulus to produce a kindling fluorescent protein label, and
CC exciting the kindling fluorescent protein label with light and
CC detecting any fluorescence from it to detect the entity. The method
CC monitors the movement of the entity. The fluorescent proteins and the
CC cDNA encoding them are useful in labeling protocols, e.g., labeling
CC proteins, organelles, cells and organisms, as biological labels or
CC markers, in protein labeling or tagging applications. The fluorescent
CC kindling proteins are useful as detectable labels, as labels in analyte
CC detection assays, in fluorescence resonance energy transfer (FRET)
CC applications, in bioluminescence resonance energy transfer (BRET)
CC applications, as biosensors in prokaryotic and eukaryotic cells, in
CC applications involving the automated screening of arrays of cells
CC expressing fluorescent reporting groups, in high through-put screening
CC assays, as second messenger detectors, and in fluorescent activated cell
CC sorting assays

XX SQ Sequence 760 BP; 208 A; 167 C; 193 G; 192 T; 0 U; 0 Other;

Query Match 63.6%; Score 436.6; DB 10; Length 760;

Best Local Similarity 77.5%; Pred. No. 1e-67;

Matches 529; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

Qy 5 TGAGCGGCGCTGCTGAAGGAGAGTATGCGCATCAGATGTACATGGAGGGGCGCCGTGACG 64
Db 78 TGGCTGGTTTGTGAAAGAAAGTATGCGCATCAAGATGTACATGGAGGGGCGCGTTAATG 137
Qy 65 GCACCTACTTCAAGTGCAGGGCGAGGGCGGACCGCAACCCCTTCGCGGGACCCAGAGCA 124
Db 138 GCATTATTTCAAGTGTGAAGGAGGAGGAGCGGCACCCATTTCGAGGTACGCGAGCA 197
Qy 125 TGAGAATCCAGTACCAGAGGGCGCCCTCGCCCTTCGCCCTTCGACATCTCTGCGCCCT 184
Db 198 TGAGGATTCATGTCAACCGAAGGGGCTCCATTACCATTTGCGCTTCGACATTTTGGC 257
Qy 185 GCTGCGAGTACGGCAGCAGGACCTTCGTGCACCAACCGCGAGATCCCGACTTCTTCA 244
Db 258 GTTGTGAGTACGGCAGCAGGACCTTTGCCACCATACGCGAGAGATTCGCCATTTCTTCA 317
Qy 245 AGCAGAGCTTCCCGAGGGGCTTCACCTGGGAGAGAACCCACCCTACGAGAGCGCGGCA 304
Db 318 AGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACCAACCACTATGAGATGGAGCA 377
Qy 305 TCCTGACCGCCCAACAGGACACCGCTGGAGGGCACTGCTGATCTACAGGTGAGG 364
Db 378 TTCTTACTGCTCATCAGGACCAAGCCTGGAGGGGAACTGCCCTTATATACAGGTGAAG 437
Qy 365 TGCACGGCAACCAACTTCCCGCGGACCGGCGCCCGTGTATGAAGAACCAAGAGCGCGCTGG 424
Db 438 TCCTTGGTACCAATTTTCTGCTGATGCGCCCGTGTATGAAGAACCAATACGAGGATGG 497
Qy 425 AGCCGAGCAGCGAGTGTGTACCCCGAGAGCGGGTCTGTGGCGCGGACCTGATGG 484
Db 498 AGCCAAAGCACTGAGTGGTGTATTCAGAGAAATGSGTCTCTGTGGAGCTGAGGTGAGG 557
Qy 485 CCCTGAAGGTGGGCGACCGGACACCTGATCTGCCCACTACACAGCTACCGGAGCAAGA 544
Db 558 CCCTTAAAGTCGGTGTATGCTGCTTTGATCTGCCATCACTATCTTCTTACAGGTCCAAGA 617
Qy 545 AGCGGTGGCGCCCTGACACCATGCCCGGCTTCCACTTACCAGCATCCGGCTCCAGATGC 604

Db 618 AAGCAGTCGCTGCTTGACAAATGCCAGGATTTTCATTTTACAGACCACCGCCTTCAGATGC 677
QY 605 TCGCGAAGAGAGACAGTACTTCGAGCTGTACAGGCGCAGCGGTGCGCGGTACAGCG 664
Db 678 GGAGGAAAGAGAGACAGTACTTTGAACCTGTACGAGCATCTGTGGTAGGTACAGTG 737
QY 665 ACCTCCCGAGAGCGCACTGA 687
Db 738 ATCTTCCTGAAAGCAAAATGA 760

RESULT 15
ABL41167
ID ABL41167 standard; cDNA; 910 BP.
XX
AC ABL41167;
XX
DT 12-AUG-2002 (first entry)
XX
DE H. crista chromoprotein wild-type base isoform hcFP640 cDNA sequence.
XX
KW Stichodactylidaen; chromoprotein; fluorescent; anthozoan; food; FRET;
KW colouring agent; pharmaceutical; cosmetic; immunoassay; biosensor; gene;
KW fluorescence resonance energy transfer; gene expression; hcFP640; ss.
XX
OS Heteractis crispa.
XX
FH Key Location/Qualifiers
FT CDS 82..765
FT /*tag= a
FT /product= "chromoprotein"
XX
PN WO200230965-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032080.
XX
PR 12-OCT-2000; 2000US-0240018P.
PR 16-JUL-2001; 2001US-0306131P.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov SA, Fradkov AF, Lukyanov KA, Gurskaya NG;
XX
WPI; 2002-444170/47.
DR P-PSDB; ABB07989.
XX
PT Novel nucleic acid encoding Stichodactylidaen chromoprotein and its
PT fluorescent mutant useful as coloring agent, labels in analyte detection
PT assays, markers in recombinant DNA applications and filters in
PT sunscreens.
XX
PS Claim 5; Fig 1; 81pp; English.
XX
CC The invention relates to a nucleic acid present in other than its natural
CC environment and encoding an Stichodactylidaen chromoprotein or its
CC fluorescent mutant, where the fluorescent protein has an emission maximum
CC ranging from 580-660 nm. The polynucleotides and encoded proteins are
CC useful in applications employing a chromo or fluorescent nucleic acid or
CC protein. Recombinant vectors comprising the nucleic acid is useful for
CC producing an Anthozoan chromo and/or fluorescent protein. The
CC chromoproteins, and their fluorescent mutants are useful as colouring
CC agents capable of imparting colour or pigment to a particular composition
CC of matter. The chromoproteins can be incorporated into a variety of
CC different compositions including food compositions, pharmaceuticals,
CC cosmetics, living organisms, e.g. animals and plants, and as labels in
CC analyte detection assays, e.g. assays for biological analytes of
CC interest. The chromoproteins may be incorporated into adducts with
CC analyte specific antibodies or their binding fragments and subsequently
CC employed in immunoassays for analytes of interest in a complex sample.
CC They are also useful as selectable markers in recombinant DNA
CC applications, e.g. the production of transgenic cells and organisms, in

CC sunscreens, as selective filters, and in fluorescence resonance energy
CC transfer (FRET) applications, where the proteins serve as donor and/or
CC acceptors in combination with a second fluorescent protein or dye, e.g. a
CC fluorescent protein. The proteins also find use as biosensors in
CC prokaryotic and eukaryotic cells, e.g. as Ca²⁺ ion indicator, as pH
CC indicator, as phosphorylation indicator, as an indicator of other ions,
CC e.g. magnesium, sodium, potassium, chloride and halides and in
CC applications involving the automated screening of arrays of cells
CC expressing fluorescent reporting groups by using microscopic imaging and
CC electronic analysis. Screening can be used for drug discovery and in the
CC field of functional genomics e.g. where the subject proteins are used as
CC markers of whole cells to detect changes in multicellular reorganisation
CC and migration, e.g. formation of multicellular tubules by endothelial
CC cells, migration of cells, wound healing and neurite outgrowth. The
CC fluorescent protein also finds use in high throughput screening assays,
CC in fluorescence activated cell sorting applications, as a label to mark a
CC population of cells, as in vivo marker in animals, in protease cleavage
CC assays, in assays to determine the phospholipid composition in biological
CC membranes and as a fluorescent timer, in which the switch of one
CC fluorescent colour to another (e.g. green to red) concomitant with the
CC aging of the fluorescent protein is used to determine the activation/
CC deactivation of gene expression, e.g. developmental gene expression, cell
CC cycle dependent gene expression or circadian rhythm specific gene
CC expression. The present sequence represents the H. crista wild-type base
CC isoform hcFP640 (hcCP) cDNA encoding a chromoprotein
XX
SQ Sequence 910 BP; 250 A; 199 C; 212 G; 249 T; 0 U; 0 Other;
Query Match 63.3%; Score 435; DB 6; Length 910;
Best Local Similarity 77.3%; Pred. No. 1.9e-67;
Matches 528; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 5 TGAGCGGCGCTGTGAAGGAGAGTATGCGCATCAAGATGTACATGAGGCGCACCGTGAACG 64
Db 83.TGCTGGTTTGTGAAAGAAATATGCGCATCAAGATGTACATGAGGCGCACCGTGAACG 142
QY 65 GCACCTACTTCAAGTCGAGGCGGAGCGGACGCAACCCCTTCGCCGCGCACCCAGAGCA 124
Db 143 GCATTTATTTCAAGTGTGAAGGAGGAGAGCGGCAACCCATTTACAGGTACGACAGCA 202
QY 125 TGAGATCCACGTACCGAGGCGCGCCCTTCGCCCTTCGACATCTCGGCCCT 184
Db 203 TGAGGATTCATGTCCCGAAGGGGCTCCATTTACCATTTTGCCTTCGACATTTGGCACCCT 262
QY 185 GCTGCGAGTACGCGACGAGGACCTTTGCTGACACACACCGCGAGATCCCCGACTTCTTCA 244
Db 263 GTTGTGAGTACGCGACGAGGACCTTTGCTGACACACATACGCGAGATTCGCGATTTCTCA 322
QY 245 AGCAGAGCTTCCCGAGGCGCTTCACCTGGGAGAGAACACACCTACGAGGACGCGCA 304
Db 323 AGCAGTCTTTCCCTGAAGGCTTTACTTGGGAAAGAACACACCTATGAAGATGGAGCA 382
QY 305 TCTTGACCGCCACCGAGGACACAGCTGGAGGCGCACTGCTGATCTACAGGTGAAGG 364
Db 383 TTCTTACTGCTCATCAGGACACAGCTGGAGGCGACTGCTTATATACAGGTGAAG 442
QY 365 TGACGCGCACCAACTTCCCGCGAGCGCGCTGATGAAGAACAGAGCGCGCGTGG 424
Db 443 TCTTTGGTACCAATTTCTCTGTGATGCGCGCTGATGAAGAACAAATCAGAGGATGG 502
QY 425 AGCCGACGACCGAGGTGGTGTACCCGAGAGCGGCTGTGCGCGCGGACGATGG 484
Db 503 AGCCATGCACTGAGGTGGTGTATCAGAGATGGTGTCTGTGTGACGATATGATGG 562
QY 485 CCTGAAGTGGCGGACCGGACCTGATGTGCCACCTACACAGCTACCGAGCAAGA 544
Db 563 CCTTAAAGTCGGTGTATCGTCTGTGATCTGCGCATCTCTATCTTCTTACAGGTCCAAGA 622
QY 545 AGCGCTGCGCGCCCTGACCATTCGCGGCTTCCATCTTACCGACATCCGCTCCAGATGC 604
Db 623 AAGCAGTCCGCTTGAACAATGCCAGGATTTTCATTTTACAGACATCCGCTTCAGATGC 682
QY 605 TCGGGAAGAAGAGGACGAGTACTTTCGAGCTGTACGAGGCGCGCGTGGCCGCTACAGCG 664

Db	683	CGAGGAAACGAAAGACGAGTACTTGA	ACTGTACGAAGCATCTGTGGCTAGGTACAGTG	742
Qy	665	ACCTGCCCGAGAGGCCAACTGA	687	
Db	743	ATCTTCTGTGAAAAAGCAAATTGA	765	

Search completed: December 10, 2004, 19:46:30
Job time : 3703 secs


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QY      241  TTCAAGCAGAGGTTCCCGAGGGCTTACCTGGAGAGAACCAACCACTACGAGACGGC 300
Db      241  TTCAAGCAGAGGTTCCCGAGGGCTTACCTGGAGAGAACCAACCACTACGAGACGGC 300
QY      301  GGATCTTGAAGCCACACAGACACAGCTGAGGGCAACTGCTGATCTACAAGGTG 360
Db      301  GGATCTTGAAGCCACACAGACACAGCTGAGGGCAACTGCTGATCTACAAGGTG 360
QY      361  AAGGTGCAACGGACCAAACTTCCCGCCGACCGGCCCGCTGATGAAGAAACAAGAGCGGGGC 420
Db      361  AAGGTGCAACGGACCAAACTTCCCGCCGACCGGCCCGCTGATGAAGAAACAAGAGCGGGGC 420
QY      421  TGGAGCCACAGACCGAGGTGGTGTACCCGAGAACGGCGTGTGTGGCGCGGAAAGGTG 480
Db      421  TGGAGCCACAGACCGAGGTGGTGTACCCGAGAACGGCGTGTGTGGCGCGGAAAGGTG 480
QY      481  ATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCACTACACAGCTACCGGAGC 540
Db      481  ATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCACTACACAGCTACCGGAGC 540
QY      541  AAGAGGCGGTGCGCGCCCTGACCATGCCCGCTTCCACTTCAACGACATCCGGCTCCAG 600
Db      541  AAGAGGCGGTGCGCGCCCTGACCATGCCCGCTTCCACTTCAACGACATCCGGCTCCAG 600
QY      601  ATGCTGCGGAGAGAGAGGAGGAGTCTTCCAGCTGTACGAGGCGAGCGTGGCCCGGTAC 660
Db      601  ATGCTGCGGAGAGAGAGGAGGAGTCTTCCAGCTGTACGAGGCGAGCGTGGCCCGGTAC 660
QY      661  AGCGACCTGCCCGAGAGGCCAACTGA 687
Db      661  AGCGACCTGCCCGAGAGGCCAACTGA 687

RESULT 2
LOCUS      AX527900                      687 bp          DNA          linear          PAT 21-NOV-2002
DEFINITION Sequence 13 from Patent WO0230965.
ACCESSION  AX527900
VERSION     AX527900.1  GI:25172349
KEYWORDS   Heteractis crispa (leathery sea anemone)
SOURCE      Heteractis crispa
ORGANISM    Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
            Stichodactylidae; Heteractis.
REFERENCE   1
AUTHORS     Lukyanov, S.A., Pradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
TITLE       Nucleic acids encoding stichodactylidae chromoproteins
JOURNAL     Patent: WO 0230965-A 13 18-APR-2002;
            Clontech Laboratories Inc. (US)
FEATURES    Location/Qualifiers
             1..687
             /organism="Heteractis crispa"
             /mol_type="unassigned DNA"
             /db_xref="taxon:175771"

ORIGIN
Query Match          97.7%; Score 671; DB 6; Length 687;
Best Local Similarity 98.5%; Pred. No. 4e-77;
Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1  ATGTGAGCGGCTCTCAAGAGAGTATGCGCATCAGATGATACATGAGGGGACCGGTG 60
Db      1  ATGTGAGCGGCTCTCAAGAGAGTATGCGCATCAGATGATACATGAGGGGACCGGTG 60
QY      61  AACGCCCACTACTTCAAGTGGAGGGCGAGGGCGAGCGCAACCCCTTTCGCGGCAACCCAG 120
Db      61  AACGCCCACTACTTCAAGTGGAGGGCGAGGGCGAGCGCAACCCCTTTCGCGGCAACCCAG 120
QY      121  AGCATGAGAAATCCAGTACCGAGGGCGCCCGCTTCGCTTCGACATCTCTGGCC 180
Db      121  AGCATGAGAAATCCAGTACCGAGGGCGCCCGCTTCGCTTCGACATCTCTGGCC 180

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QY      181  CCTGCTGAGTACGGAGAGAGGACCTTCTGTGACCAACACCGCGGAGATCCCGACTTC 240
Db      181  CCTGCTGAGTACGGAGAGAGGACCTTCTGTGACCAACACCGCGGAGATCCCGACTTC 240
QY      241  TTCAAGCAGAGGTTCCCGAGGGCTTACCTGGAGAGAACCAACCACTACGAGACGGC 300
Db      241  TTCAAGCAGAGGTTCCCGAGGGCTTACCTGGAGAGAACCAACCACTACGAGACGGC 300
QY      301  GGATCTTGAAGCCACACAGACACAGCTGAGGGCAACTGCTGATCTACAAGGTG 360
Db      301  GGATCTTGAAGCCACACAGACACAGCTGAGGGCAACTGCTGATCTACAAGGTG 360
QY      361  AAGGTGCAACGGACCAAACTTCCCGCCGACCGGCCCGCTGATGAAGAAACAAGAGCGGGGC 420
Db      361  AAGGTGCAACGGACCAAACTTCCCGCCGACCGGCCCGCTGATGAAGAAACAAGAGCGGGGC 420
QY      421  TGGAGCCACAGACCGAGGTGGTGTACCCGAGAACGGCGTGTGTGGCGCGGAAAGGTG 480
Db      421  TGGAGCCACAGACCGAGGTGGTGTACCCGAGAACGGCGTGTGTGGCGCGGAAAGGTG 480
QY      481  ATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCACTACACAGCTACCGGAGC 540
Db      481  ATGGCCCTGAAGTGGGCGACCGGACCTGATCTGCCACCACTACACAGCTACCGGAGC 540
QY      541  AAGAGGCGGTGCGCGCCCTGACCATGCCCGCTTCCACTTCAACGACATCCGGCTCCAG 600
Db      541  AAGAGGCGGTGCGCGCCCTGACCATGCCCGCTTCCACTTCAACGACATCCGGCTCCAG 600
QY      601  ATGCTGCGGAGAGAGAGGAGGAGTCTTCCAGCTGTACGAGGCGAGCGTGGCCCGGTAC 660
Db      601  ATGCTGCGGAGAGAGAGGAGGAGTCTTCCAGCTGTACGAGGCGAGCGTGGCCCGGTAC 660
QY      661  AGCGACCTGCCCGAGAGGCCAACTGA 687
Db      661  AGCGACCTGCCCGAGAGGCCAACTGA 687

RESULT 3
LOCUS      AX527902                      1396 bp          DNA          linear          PAT 21-NOV-2002
DEFINITION Sequence 15 from Patent WO0230965.
ACCESSION  AX527902
VERSION     AX527902.1  GI:25172350
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Lukyanov, S.A., Pradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
TITLE       Nucleic acids encoding stichodactylidae chromoproteins
JOURNAL     Patent: WO 0230965-A 15 18-APR-2002;
            Clontech Laboratories Inc. (US)
FEATURES    Location/Qualifiers
             1..1396
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="fusion construct"

ORIGIN
Query Match          97.7%; Score 671; DB 6; Length 1396;
Best Local Similarity 98.5%; Pred. No. 3.5e-77;
Matches 677; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      1  ATGTGAGCGGCTCTCAAGAGAGTATGCGCATCAGATGATACATGAGGGGACCGGTG 60
Db      710  ATGTGAGCGGCTCTCAAGAGAGTATGCGCATCAGATGATACATGAGGGGACCGGTG 769
QY      61  AACGCCCACTACTTCAAGTGGAGGGCGAGGGCGAGCGCAACCCCTTTCGCGGCAACCCAG 120
Db      770  AACGCCCACTACTTCAAGTGGAGGGCGAGGGCGAGCGCAACCCCTTTCGCGGCAACCCAG 829
QY      121  AGCATGAGAAATCCAGTACCGAGGGCGCCCGCTTCGCTTCGACATCTCTGGCC 180

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Db 830 AGCATCGGATCCAGTACCGAGGGCGCCCTTCGCTTCGATCCTGGCC 889
QY 181 CCCTGCTCGAGTACGGCAGAGACCTTCGTGACACACACCGCGAGATCCCGACTTC 240
Db 890 CCCTGCTCGAGTACGGCAGAGACCTTCGTGACACACACCGCGAGATCCCGACTTC 949
QY 241 TTCAGCAGAGCTTCCCGAGGGTTTCACTGGGAGAGAACCACTACGAGAGCGGC 300
Db 950 TTCAGCAGAGCTTCCCGAGGGTTTCACTGGGAGAGAACCACTACGAGAGCGGC 1009
QY 301 GGCTTCCTGAGCCGACCGAGACACAGCTGAGGGCACTGCTGTATCAAGGTG 360
Db 1010 GGCTTCCTGAGCCGACCGAGACACAGCTGAGGGCACTGCTGTATCAAGGTG 1069
QY 361 AAGGTGACCGACCACTTCCCGCGGACCGGCTGTATGAGAGAACAGAGCGGCGGC 420
Db 1070 AAGGTGTCGGCACCACTTCCCGCGGACCGGCTGTATGAGAGAACAGAGCGGCGGC 1129
QY 421 TGGAGGCCACGACCGAGGTGTATCCCGAGAACCGGCTGTGTCGGCGGGAAGCTG 480
Db 1130 TGGAGGCCACGACCGAGGTGTATCCCGAGAACCGGCTGTGTCGGCGGGAAGCTG 1189
QY 481 ATGGCCCTGAGGTGGGCGACCGGCACTGTATGTCACCACTACACGACTACCGGAGC 540
Db 1190 ATGGCCCTGAGGTGGGCGACCGGCGTGTATGTCACCACTACACGACTACCGGAGC 1249
QY 541 AAGAGGCGCTGCGCGCCCTGACATGCGCGGCTTCACTTACCGACATCCGCGTCCAG 600
Db 1250 AAGAGGCGCTGCGCGCCCTGACATGCGCGGCTTCACTTACCGACATCCGCGTCCAG 1309
QY 601 ATGCTGCGGAAGAGAGGACGACTTCTGAGCTGTACGAGGCGGCGTGGCCCGGTAC 660
Db 1310 ATGCTGCGGAAGAGAGGACGACTTCTGAGCTGTACGAGGCGGCGTGGCCCGGTAC 1369
QY 661 AGCGACCTGCCGAGAGGCGCAACTGA 687
Db 1370 AGCGACCTGCCGAGAGGCGCAACTGA 1396

RESULT 4
AX527904
LOCUS AX527904 1424 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 17 from Patent WO0230965.
ACCESSION AX527904
VERSION AX527904.1 GI:25172351
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Lukyanov, S.A., Fradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
TITLE Nucleic acids encoding stichodactylidae chromoproteins
JOURNAL Patent: WO 0230965-A 17 18-APR-2002;
Clontech Laboratories Inc. (US)
FEATURES
source
1. .1424
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion construct"

ORIGIN
Query Match 97.4%; Score 669.4; DB 6; Length 1424;
Best Local Similarity 98.4%; Pred. No. 5.5e-77;
Matches 676; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGTGAGCGGCTGCTGAAGGAGAGTATGGCATCAAGATGATACATGGAGGCGCGGTG 60
Db 14 ATGGTGAGCGGCTGCTGAAGGAGAGTATGGCATCAAGATGATACATGGAGGCGCGGTG 73
QY 61 AACGGCCACTACTTCAAGTGGAGGCGGAGGCGGCAACCCCTTCGCGGCGACCCAG 120

Db 74 AACGGCCACTACTTCAAGTGGAGGCGGAGCGCAACCCCTTCGCGGCGACCCAG 133
QY 121 AGCATGAGATCCAGTACCGAGGGCGCCCTTCGCTTCGATCCTGGCC 180
Db 134 AGCATCGGATCCAGTACCGAGGGCGCCCTTCGCTTCGATCCTGGCC 193
QY 181 CCCTGCTCGAGTACGGCAGAGACCTTCGTGACACACCGCGAGATCCCGACTTC 240
Db 194 CCCTGCTCGAGTACGGCAGAGACCTTCGTGACACACCGCGAGATCCCGACTTC 253
QY 241 TTCAGCAGAGCTTCCCGAGGGTTTCACTGGGAGAGAACCACTACGAGAGCGGC 300
Db 254 TTCAGCAGAGCTTCCCGAGGGTTTCACTGGGAGAGAACCACTACGAGAGCGGC 313
QY 301 GGCTTCCTGAGCCGACCGAGACACAGCTGAGGGCACTGCTGTATCAAGGTG 360
Db 314 GGCTTCCTGAGCCGACCGAGACACAGCTGAGGGCACTGCTGTATCAAGGTG 373
QY 361 AAGGTGACCGACCACTTCCCGCGGACCGGCTGTATGAGAGAACAGAGCGGCGGC 420
Db 374 AAGGTGCTGGCACCACTTCCCGCGGACCGGCTGTATGAGAGAACAGAGCGGCGGC 433
QY 421 TGGAGGCCACGACCGAGGTGTATCCCGAGAACCGGCTGTGTCGGCGGGAAGCTG 480
Db 434 TGGAGGCCACGACCGAGGTGTATCCCGAGAACCGGCTGTGTCGGCGGGAAGCTG 493
QY 481 ATGGCCCTGAGGTGGGCGACCGGCACTGTATGTCACCACTACACGACTACCGGAGC 540
Db 494 ATGGCCCTGAGGTGGGCGACCGGCGTGTATGTCACCACTACACGACTACCGGAGC 553
QY 541 AAGAGGCGCTGCGCGCCCTGACATGCGCGGCTTCACTTACCGACATCCGCGTCCAG 600
Db 554 AAGAGGCGCTGCGCGCCCTGACATGCGCGGCTTCACTTACCGACATCCGCGTCCAG 613
QY 601 ATGCTGCGGAAGAGAGGACGACTTCTGAGCTGTACGAGGCGGCGTGGCCCGGTAC 660
Db 614 ATGCTGCGGAAGAGAGGACGACTTCTGAGCTGTACGAGGCGGCGTGGCCCGGTAC 673
QY 661 AGCGACCTGCCGAGAGGCGCAACTGA 687
Db 674 AGCGACCTGCCGAGAGGCGCAACTGA 700

RESULT 5
AX527894
LOCUS AX527894 681 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 7 from Patent WO0230965.
ACCESSION AX527894
VERSION AX527894.1 GI:25172346
KEYWORDS Heteractis crispa (leathery sea anemone)
SOURCE Heteractis crispa
ORGANISM Heteractis crispa
REFERENCE 1
AUTHORS Lukyanov, S.A., Fradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
TITLE Nucleic acids encoding stichodactylidae chromoproteins
JOURNAL Patent: WO 0230965-A 7 18-APR-2002;
Clontech Laboratories Inc. (US)
FEATURES
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1. .681
/organism="Heteractis crispa"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 64.2%; Score 441.2; DB 6; Length 681;
Best Local Similarity 78.2%; Pred. No. 1.2e-47;
Matches 530; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

QY 10 GGCCTGCTGAAGGAGAGTATGGCATCAAGATGATGATGAGGCGGCGCATCGGCCAC 69
Db 4 GCTTTTGAAGAAAGTATGGCATCAAGATGATGATGAGGCGGCGCATCGGCCAT 63

QY 70 TACTTCAAGTGGAGGGGCGAGCGGCGAAGCCCTTCCGCGCACCCAGAGCATGAGA 129
 Db 64 TATTTCAAAGTGTGAAGGAGGAGAGAGCGGCAACCCATTTCGAGGTACGAGAGCATGAGG 123
 QY 130 ATCCACGTGACCGAGGGGCGCCCTGCTCCCTTCGCTTCGACATCTCGGCCCCCTGCTGC 189
 Db 124 ATTATGTCACCGAAGGGCTCCATTACCAATTCGCTTCGACATTTTGGCACCGTGTGT 183
 QY 190 GAGTACGGCAGAGGACCTTCGTGTCACACACCGCCGAGATCCCGACTTCTTCAAGCAG 249
 Db 184 GAGTACGGCAGAGGACCTTTGTCCACCATACGCGAGAGATTCGCGATTCTTCAAGCAG 243
 QY 250 AGCTTCCCGAGGGCTTCACCTGGGAGAGAACCAACCTACGAGGACGGCGGCATCTG 309
 Db 244 TCTTTCCTGAAGGCTTACTTGGGAAGAACCAACCTATGAAGTGAAGGCATCTT 303
 QY 310 ACCGCCACACGAGACACAGCCTGGAGGGCAACTGCTGTATCTTAAAGGTGAAGGTGCAC 369
 Db 304 ACTGCTCATCAGGACACAAAGCTGGAGGGAACTGCTTATATACAAAGGTGAAGTCTT 363
 QY 370 GGCACCAACTTCCCGCGAGCGCCGCTGTATGAAGAACAGACGCGCGCTGGAGGCC 429
 Db 364 GGTACCAATTTCTCTGCTGATGGCCCGCTGATGAAGAACAAATCAGAGGATGGAGCCA 423
 QY 430 AGCACCGAGGTGTGTACCCCGAGAACCGCGTGTGTCGCGCCGGAACGTGATGGCCCTG 489
 Db 424 AGCACTGAGGTGTGTATCCAGAGAAATGTGCTGCTGTGGACGTAATGTGATGGCCCTT 483
 QY 490 AAGTGGGGACCGCACCTGATCTGCCACCACTACACGACTACCGGACGAGAGGCC 549
 Db 484 AAGTCGCTGATCGTGTGTTGATCTGCCATCACTATATCTTCTACAGGTCCAGAAAGCA 543
 QY 550 GTGCGCGCTTCACCATCCCGGCTTCCACTTCCAGACATCCGCTCCAGATGCTCGG 609
 Db 544 GTCCGCTCTTCAACATCCAGGATTTCAATTTACAGACATCCGCTTCAGATGCTGAGG 603
 QY 610 AAGAAGAAGGACGAGTACTTCGAGCTGTACAGGCGCAGCGTGGCCGCTACAGGACCTG 669
 Db 604 AAAGAGAAGACGAGTACTTTGAATGTGTACGAAGCATCTGTGGCTAGGTACAGTATCTT 663
 QY 670 CCGGAGAGGCCAACTGA 687
 Db 664 CCTGAAAAGCAATTTGA 681

RESULT 6
 LOCUS AX527896 681 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 9 from Patent WO0230965.
 ACCESSION AX527896
 VERSION AX527896.1 GI:25172347
 KEYWORDS
 SOURCE Heteractis crispa (leathery sea anemone)
 ORGANISM Heteractis crispa
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 Stichodactylidae; Heteractis.
 REFERENCE 1
 AUTHORS Lukyanov, S.A., Pradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
 TITLE Nucleic acids encoding stichodactylidae chromoproteins
 JOURNAL Patent: WO 0230965-A 9 18-APR-2002;
 Clontech Laboratories Inc. (US)
 FEATURES
 Location/Qualifiers
 1..681
 /organism="Heteractis crispa"
 /mol_type="unassigned DNA"
 /db_xref="taxon:175771"
 ORIGIN
 Query Match 64.0%; Score 439.6; DB 6; Length 681;
 Best Local Similarity 78.0%; Pred. No. 2e-47;
 Matches 529; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 10 GGCCTGCTGAAGGAGATATGCGATCAAGATGTACATGGAGGCAACCGTGAACGGCCAC 69
 Db 4 GGTGTTGTTGAAGAAGATATGCGATCAAGATGTACATGGAGGCAACCGTGAATGGCCAT 63
 QY 70 TACTTCAAGTGGAGGGGCGAGCGGCAACCCCTTCGCGCACCCAGAGCATGAGA 129
 Db 64 TATTTCAAAGTGTGAAGGAGGAGAGCGGCAACCCATTTCGAGGTACGAGAGCATGAGG 123
 QY 130 ATCCACGTGACCGAGGGGCGCCCTGCTCCCTTCGCTTCGACATCTCGGCCCCCTGCTGC 189
 Db 124 ATTATGTCACCGAAGGGCTCCATTACCAATTCGCTTCGACATTTTGGCACCGTGTGT 183
 QY 190 GAGTACGGCAGAGGACCTTCGTGTCACACACCGCCGAGATCCCGACTTCTTCAAGCAG 249
 Db 184 GGTACGGCAGAGGACCTTTGTCCACCATACGCGAGAGATTCGCGATTCTTCAAGCAG 243
 QY 250 AGCTTCCCGAGGGCTTCACCTGGGAGAGAACCAACCTACGAGGACGGCGGCATCTG 309
 Db 244 TCTTTCCTGAAGGCTTACTTGGGAAGAACCAACCTATGAAGTGAAGGCATCTT 303
 QY 310 ACCGCCACACGAGACACAGCCTGGAGGGCAACTGCTGTATCTTAAAGGTGAAGGTGCAC 369
 Db 304 ACTGCTCATCAGGACACAAAGCTGGAGGGAACTGCTTATATACAAAGGTGAAGTCTT 363
 QY 370 GGCACCAACTTCCCGCGAGCGCCGCTGTATGAAGAACAGACGCGCGCTGGAGGCC 429
 Db 364 GGTACCAATTTCTCTGCTGATGGCCCGCTGATGAAGAACAAATCAGAGGATGGAGCCA 423
 QY 430 AGCACCGAGGTGTGTACCCCGAGAACCGCGTGTGTCGCGCCGGAACGTGATGGCCCTG 489
 Db 424 AGCACTGAGGTGTGTATCCAGAGAAATGTGCTGCTGTGGACGTAATGTGATGGCCCTT 483
 QY 490 AAGTGGGGACCGCACCTGATCTGCCACCACTACACGACTACCGGACGAGAGGCC 549
 Db 484 AAGTCGCTGATCGTGTGTTGATCTGCCATCACTATATCTTCTACAGGTCCAGAAAGCA 543
 QY 550 GTGCGCGCTTCACCATCCCGGCTTCCACTTCCAGACATCCGCTCCAGATGCTCGG 609
 Db 544 GTCCGCTCTTCAACATCCAGGATTTCAATTTACAGACATCCGCTTCAGATGCTGAGG 603
 QY 610 AAGAAGAAGGACGAGTACTTCGAGCTGTACAGGCGCAGCGTGGCCGCTACAGGACCTG 669
 Db 604 AAAGAGAAGACGAGTACTTTGAATGTGTACGAAGCATCTGTGGCTAGGTACAGTATCTT 663
 QY 670 CCGGAGAGGCCAACTGA 687
 Db 664 CCTGAAAAGCAATTTGA 681

RESULT 7
 LOCUS AX527910 684 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 23 from Patent WO0230965.
 ACCESSION AX527910
 VERSION AX527910.1 GI:25172356
 KEYWORDS
 SOURCE Heteractis crispa (leathery sea anemone)
 ORGANISM Heteractis crispa
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 Stichodactylidae; Heteractis.
 REFERENCE 1
 AUTHORS Lukyanov, S.A., Pradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
 TITLE Nucleic acids encoding stichodactylidae chromoproteins
 JOURNAL Patent: WO 0230965-A 23 18-APR-2002;
 Clontech Laboratories Inc. (US)
 FEATURES
 Location/Qualifiers
 1..684
 /organism="Heteractis crispa"
 /mol_type="unassigned DNA"
 /db_xref="taxon:175771"
 ORIGIN
 Query Match 63.8%; Score 438.2; DB 6; Length 684;

Best Local Similarity 77.6%; Pred. No. 3e-47;
Matches 530; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 5 TGAGCGGCTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGAGGCGACCGTGAACG 64
DB |||||
2 TGGCTGGTTTGTGAAGAAAGTATGCGCATCAAGATGTACATGAGGCGACCGTGAATG 61
QY 65 GCCACTACTTCAAGTGCAGGCGGAGGCGACGCAACCCCTTCGCGCGCACCCAGAGCA 124
DB |||||
62 GCCATTATTTCAAGTGTGAAGAGAGGAGAGCGCAACCCATTTACAGGTACGAGAGCA 121
QY 125 TGAGATTCAGTGCAGGCGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTT 184
DB |||||
122 TGAGATTATGTACCGAAGGGCTCCATTACCATTTGCTTCGACATTTTGGCACCGT 181
QY 185 GCTGAGTACGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 244
DB |||||
182 GTTGTGAGTACGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 241
QY 245 AGCAGAGTTCGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 304
DB |||||
242 AGCAGTCTTTCGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 301
QY 305 TCCTGAGTTCGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 364
DB |||||
302 TTCCTTACTGCTCATCAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 361
QY 365 TGCAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 424
DB |||||
422 AGCCAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 481
QY 485 CCCTGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 544
DB |||||
542 AGCAGTTCGCGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 601
QY 605 TCGGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 664
DB |||||
602 CGAGGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 661
QY 665 ACCTGCGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 687
DB |||||
662 ATCTTCTGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 684

RESULT 8
AX527892
LOCUS AX527892 684 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 5 from Patent WO0230965.
ACCESSION AX527892
VERSION AX527892.1 GI:25172345
KEYWORDS Heteractis crispa (leathery sea anemone)
SOURCE Heteractis crispa
ORGANISM Heteractis crispa
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Stichodactylidae; Heteractis.
1
REFERENCE
AUTHORS Lukyanov,S.A., Pradkov,A.F., Lukyanov,K.A. and Gurskaya,N.G.
TITLE Nucleic acids encoding stichodactylidae chromoproteins
JOURNAL Patent: WO 0230965-A 5 18-APR-2002;
Clontech Laboratories Inc. (US)
FEATURES
source Location/Qualifiers
1..684
/organism="Heteractis crispa"
/mol_type="unassigned DNA"
/db_xref="taxon:175771"

ORIGIN

Query Match 63.6%; Score 436.6; DB 6; Length 684;
Best Local Similarity 77.5%; Pred. No. 4.8e-47;
Matches 529; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 5 TGAGCGGCTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGAGGCGACCGTGAACG 64
DB |||||
2 TGGCTGGTTTGTGAAGAAAGTATGCGCATCAAGATGTACATGAGGCGACCGTGAATG 61
QY 65 GCCACTACTTCAAGTGCAGGCGGAGGCGACGCAACCCCTTCGCGCGCACCCAGAGCA 124
DB |||||
62 GCCATTATTTCAAGTGTGAAGAGAGGAGAGCGCAACCCATTTACAGGTACGAGAGCA 121
QY 125 TGAGATTCAGTGCAGGCGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTT 184
DB |||||
122 TGAGGATTATGTACCGAAGGGCTCCATTACCATTTGCTTCGACATTTTGGCACCGT 181
QY 185 GCTGCGAGTACGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 244
DB |||||
182 GTTGTGAGTACGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 241
QY 245 AGCAGAGTTCGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 304
DB |||||
242 AGCAGTCTTTCGCGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 301
QY 305 TCTGACCGGCGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 364
DB |||||
302 TTCCTTACTGCTCATCAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 361
QY 365 TGCAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCCTTCTTCA 424
DB |||||
362 TCTTGGTACCATTTTCTGCTGATGCGCCGCTGATGAGAACAAATACAGGAGATGG 421
QY 425 AGCCAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 484
DB |||||
422 AGCCAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 481
QY 485 CCCTGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 544
DB |||||
482 CCCTTAAAGTCGCTGATGCTGCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 541
QY 545 AGGCGGTGCGCCCTTCGATGCTGCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 604
DB |||||
542 AAGCAGTTCGCTTCGATGCTGCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 601
QY 605 TCGCGGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 664
DB |||||
602 CGAGGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 661
QY 665 ACCTGCGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 687
DB |||||
662 ATCTTCTGAGGAGGAGGAGGAGGCGCCCTTCGCTTCGATCTCGACATCTGCGCCGGAACGTGATGG 684

RESULT 9
AF363776
LOCUS AF363776 908 bp mRNA linear INV 05-NOV-2001
DEFINITION Heteractis crispa GFP-like chromoprotein mRNA, complete cds.
ACCESSION AF363776
VERSION AF363776.1 GI:16660115
KEYWORDS Heteractis crispa (leathery sea anemone)
SOURCE Heteractis crispa
ORGANISM Heteractis crispa
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Stichodactylidae; Heteractis.
1 (bases 1 to 908)
REFERENCE
AUTHORS Gurskaya,N.G., Pradkov,A.F., Tersikh,A., Matz,M.V., Labas,V.A.,
Martyanov,V.I., Yanushevich,I.G., Lukyanov,K.A. and Lukyanov,S.A.
TITLE GFP-like chromoproteins as a source of far-red fluorescent proteins
JOURNAL FEBS Lett. 507 (1), 16-20 (2001)
MEDLINE 21538626
PUBMED 11692051

REFERENCE 2 (bases 1 to 908)
AUTHORS Gurskaya,N.G., Lukyanov,K.A., Labas,Y.A. and Lukyanov,S.A.
TITLE Direct Submission
JOURNAL Miklukho-Maklaya 16/10, Moscow 117997, Russia
FEATURES
source
1. 908
/organism="Heteractis crispa"
/mol_type="mRNA"
/db_xref="taxon:175771"
77.760
/note="hccp"
/codon_start=1
/product="GFP-like chromoprotein"
/protein_id="AA127538.1"
/db_xref="GI:1660116"
/translation="MAGLLKESMRIRKYMEGTVNGHYFKCEGSDGNPFRTGQSMRIH
VTEGAPUPFAFDILAPCCYSGSRFTVHHHTAEIPDFKQSPFEGFTWERITTYEDGGIL
TAHQDTSLGELIYKVLGTNPADGPNVKNKSGWEPCTEVVPEVNGVLCGRNM
ALKYGDRLICHLYTSYRSKAVRALTMPGFHFTDIRLQWPRKKDDEYFELYEASVAR
YSDLPKXAN"
ORIGIN
Query Match 63.6%; Score 436.6; DB 3; Length 908;
Best Local Similarity 77.5%; Pred. No. 4.5e-47;
Matches 529; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
QY 5 TGAGCGGCTGTGAAGGAGAGTATGCGATCAAGATGTATCATGGAGGCGACCGTGAACG 64
DB 78 TGGCTGGTTTGTGAAGAAAGTATGCGATCAGATGTATCATGGAGGCGACCGTGAATG 137
QY 65 GCCACTACTCAAGTGCAGGCGGAGGCGGACGCGAACCCCTTCGCCGCGCACCCAGAGCA 124
DB 138 GCCATTATTCAAGTGTGAAGGAGGAGGAGGAGCGCAACCCATTATACAGGTACGAGAGCA 197
QY 125 TGAGAAATCCAGTACCGGAGGCGGCGCCCTCGCCCTTCGCTTCGATCATCTGCGCCCT 184
DB 198 TGAGAAATTCATGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 257
QY 185 GTGCGAGTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 244
DB 258 GTTGTGAGTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 317
QY 245 AGCAGAGCTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 304
DB 318 AGCAGTCTTCCCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 377
QY 305 TCCTGACCGCGCCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364
DB 378 TTCTTACTGCTCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 437
QY 365 TGCACGCGACCAACTTCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
DB 438 TCCTTGGTACCAATTTTCCCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 497
QY 425 AGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 484
DB 498 AGCCATGCACTGAGGTGGTTTATCAGAGATGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTG 557
QY 485 CCCTGAAGGTGGCGGACCGGACCGTGTATCTGCGACCACTACACGAGCTACCGGAGGAGGAGG 544
DB 558 CCCTTAAAGTCGCTGATGCTG 617
QY 545 AGCCGCTGCGGCGCTGACCACTGCGCGCTTCCACTTCACCGACATCGGCTCCAGATGC 604
DB 618 AAGCACTCGGCTGTGACATGCGAGGATTTCAATTTACAGACATCGGCTTCAGATGC 677
QY 605 TGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664
DB 678 CGAGG 737
QY 665 ACCTGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 687

Db 738 ATCTTCTCTGAAAAAGCAAAATTGA 760
RESULT 10
LOCUS AX527888 910 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO0230965.
ACCESSION AX527888
VERSION AX527888.1 GI:25172343
KEYWORDS Heteractis crispa (leathery sea anemone)
SOURCE Heteractis crispa
ORGANISM Heteractis crispa
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinifera;
Stichodactylidae; Heteractis.
REFERENCE 1
AUTHORS Lukyanov,S.A., Pradkov,A.F., Lukyanov,K.A. and Gurskaya,N.G.
TITLE Nucleic acids encoding stichodactylidae chromoproteins
JOURNAL Patent: WO 0230965-A 1 18-APR-2002;
Clontech Laboratories Inc. (US)
FEATURES
source
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/organism="Heteractis crispa"
/mol_type="unassigned DNA"
/db_xref="taxon:175771"
ORIGIN
Query Match 63.3%; Score 435; DB 6; Length 910;
Best Local Similarity 77.3%; Pred. No. 7.3e-47;
Matches 528; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 5 TGAGCGGCTGTGAAGGAGAGTATGCGATCAAGATGTATCATGGAGGCGACCGTGAACG 64
DB 83 TGGCTGGTTTGTGAAGAAAGTATGCGATCAGATGTATCATGGAGGCGACCGTGAATG 142
QY 65 GCCACTACTTCAAGTGCAGGCGGAGGCGGCGCAACCCCTTCGCCGCGCACCCAGAGCA 124
DB 143 GCCATTATTCAAGTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 202
QY 125 TGAGAAATCCAGTACCGGAGGCGGCGCCCTCGCCCTTCGATCATCTGCGCCCT 184
DB 203 TGAGAAATTCATGTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 262
QY 185 GTGCGAGTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 244
DB 263 GTTGTGAGTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 322
QY 245 AGCAGAGCTTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 304
DB 323 AGCAGTCTTCCCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 382
QY 305 TCCTGACCGCGCCACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 364
DB 383 TTCTTACTGCTCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 442
QY 365 TGCACGCGACCAACTTCCCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 424
DB 443 TCCTTGGTACCAATTTTCCCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 502
QY 425 AGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 484
DB 503 AGCCATGCACTGAGGTGGTTTATCAGAGATGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTG 562
QY 485 CCCTGAAGGTGGCGGACCGGACCGTGTATCTGCGACCACTACACGAGCTACCGGAGGAGGAGG 544
DB 563 CCCTTAAAGTCGCTGATGCTG 622
QY 545 AGCCGCTGCGGCGCTGACCACTGCGCGCTTCCACTTCACCGACATCGGCTCCAGATGC 604
DB 623 AAGCACTCGGCTGTGACATGCGAGGATTTCAATTTACAGACATCGGCTTCAGATGC 682
QY 605 TGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 664
DB 683 CGAGG 742

QY	665	ACCTGCCGCGAAGCCCACTGA	67
Db	743	ATCTTCTGAAAAAGCAAAITGA	765
RESULT 11			
AX527914			
LOCUS	AX527914	910 bp	DNA
DEFINITION	Sequence 27 from Patent WO0230965.		linear
ACCESSION	AX527914		
VERSION	AX527914.1	GI:25172358	
KEYWORDS			
SOURCE	Heteractis crispa (leathery sea anemone)		
ORGANISM	Heteractis crispa		
REFERENCE			
AUTHORS	Lukyanov, S.A., Pradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.		
TITLE	Nucleic acids encoding stichodactylid chromoproteins		
JOURNAL	Patent: WO 0230965-A 27 18-APR-2002;		
FEATURES	Clontech Laboratories Inc. (US)		
Source	Location/Qualifiers		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:175771"		
ORIGIN			
Query Match	63.3%;	Score 435;	DB 6; Length 910;
Best Local Similarity	77.3%;	Pred. No. 7.3e-47;	
Matches	528; Conservative	0; Mismatches 155;	Indels 0; Gaps 0;
QY	5	TGACGGCCTGCTGAAGAGAGATGCGCATCAAGATGTACATCGAGGGCAACCGTGAACG	64
Db	83	TGGCTGCTGTTGTTGAAAGAAAGTATGGCATCAAGATGTACATGGAAGCACGCTTAATG	142
QY	65	GCCACTACTTCAAGTGGAGGGCGAGGGCGACGCAACCCCTTCGCCGGGACCCAGACGA	124
Db	143	GCCATTATTCAAGTGTGAAGAGAGGAGAGCGCAACCCATTACAGGTACGAGAGCA	202
QY	125	TGAGAAATCCAGTGACCGAGGGCGCCCTTCGCTTCGCTTCGACATCTCGACATCTGCGCCCT	184
Db	203	TGAGGATTCATGTCAACGAAAGGGCTCCATTACCATTTGCTTCGACATTTTGGCACCGT	262
QY	185	GCTGCGAGTACGGCAGCAGGACCTTCGTGCACACACCGCGAGATCCCGACTTCCTCA	244
Db	263	GTGTGAGTACGGCAGCAGGACCTTTGTCCACCATCGGACAGATTCCCGATTTCCTCA	322
QY	245	AGCAGAGCTTCCCGAGGGCTTCACTCTGGAGAGAACCCACCCTAGGAGGACCGCGGCA	304
Db	323	AGCAGCTTTTCCCTGAAGGCTTTACTTTGGGAAAGAACCAACCTATGAAGTGAAGCA	382
QY	305	TCCTGACGGCCACAGACACAGCTTGAGGGCACTGCTGATCTACAGGTGAAGG	364
Db	383	TTCTTACTGCTCATCAGGACACAGCTTGAGGGGAACTGCTTATATACAAGGTGAAG	442
QY	365	TGCACGGCACCAACTTCCCGCGGACGCGCCCTGTGATGAAGAACAGAGCGGCGGCTGGG	424
Db	443	TCCTTGATACCAATTTTCTGCTGATGCGCCCGTGATGAAGAACAAATCAGGAGATGG	502
QY	425	AGCCAGCACCGAGGTGGTGTACCCGAGAACCGCGTGTGTGGCGCGGACGACTGTATGG	484
Db	503	AGGCATGCACTGAGGTGGTTTATCCAGAGATGGTGTCTGTGTGACGTAATGTATGG	562
QY	485	CCCTGAAGGTGGGGACCGGCACCTGATCTGCCACCACTACCCAGCTACCGGAGCAAGA	544
Db	563	CCCTTAAGTCGGTGATCGTCTGTTGATCTGCCATCTCTATCTTTCACAGTCCAGA	622
QY	545	AGGCGTGGCGGCGCTGACATGCCCGGCTTCCATCTACCGACATCCGGCTCCAGATGC	604
Db	623	AAGCAGTCCGTGCTTGAATGCAATGCAAGATTTCATTTTACAGACATCCGCTTCAGATGC	682

QY 605 TCGCGAAGAAGAGGACGAGTACTTCGAGCTGTGTACGAGGCCAGGTGGCCCGGTACAGCG 660
 Db 683 CGAGGAAAAAGGAAACGAGTACTTTGAACCTGTGTACGAGCATCTGTGGCTAGGTACAGTG 742
 QY 665 ACCTGCCCGAGAGGCGCAACTGA 687
 Db 743 ATCTTCTGAAAAGCAAAATTGA 765

 RESULT 12
 AX527890 908 bp DNA linear PAT 21-NOV-2000
 LOCUS
 DEFINITION Sequence 3 from Patent WO0230965.
 ACCESSION AX527890
 VERSION AX527890.1 GI:25172344
 KEYWORDS
 ORGANISM
 SOURCE
 Heteractis crispa (leathery sea anemone)
 Heteractis crispa
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 Stichodactylidae; Heteractis.
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 REFERENCE
 AUTHORS Lukanov, S.A., Pradkov, A.F., Lukanov, K.A. and Gurskaya, N.G.
 TITLE Nucleic acids encoding stichodactylidae chromoproteins
 JOURNAL Patent: WO 0230965-A 3 18-APR-2002;
 Clontech Laboratories Inc. (US)
 FEATURES
 source
 1..908
 /organism="Heteractis crispa"
 /mol_type="unassigned DNA"
 /db_xref="taxon:175771"
 ORIGIN
 Query Match 62.9%; Score 431.8; DB 6; Length 908;
 Best Local Similarity 77.0%; Pred. No. 1.9e-46;
 Matches 526; Conservative 0; Mismatches 157; Indels 0; Gaps 0

 QY 5 TGAGCGCCCTGCTGAAGGAGAGTATGCGCATCAAGATGTACATGAGGCGCACCGTGAACG 64
 Db 78 TGCGTGGTTTGTGAAGAAAAGTATGGCCATCAAGATGTACATGGAAGGACCGGTTAATG 137
 QY 65 GCACCTACTTCAAGTGCAGGCGGAGGCGGACCGCACCCCTTCGGCGCACCCAGAGCA 124
 Db 138 GCATATATTTCAAGTGTGAAGAGAGGAGGACGCGAACCATTTACAGTACGAGAGCA 197
 QY 125 TGAGATCCACGTGACCGAGGCGCCCGCTTCGCTTTTCGATCTTCGACATCTTGGCCCTC 184
 Db 198 TGAGGATTCATGTCACCGAAGGGCTCCATTACATTTGCTTCGACATTTTGGCACCGT 257
 QY 185 GCTGCGAGTACGGCAGCAGGACCTTCGTGCACACACCGCGGAGATCCCGGACTTCTTCA 244
 Db 258 GTTGTTGAGTACGGCAGCAGGACCTTTGTCCACCATACGGCAGAGATTCGCCGATTTCTTCA 317
 QY 245 AGCAGAGCTTCCCGAGGGCTTCACTTCGGGAGAGAACACCACTTACGAGGACGGCGCA 304
 Db 318 AGCAGCTTTTCCCTGAGGCTTTACTTTGGGAAGAACCAACCTATGAGATGGAGCA 377
 QY 305 TCTGACCGCCACACAGAGACACAGCTTCGAGGCGCACTGCCTGTATCTACAGGTGAAGG 364
 Db 378 TTCTTACTGCTCATCAGGACACAAGCGCTGGAGGGGAATCGCTTTATATACAAGGTGAAAG 437
 QY 365 TGCAGGGACCAACTTCCCGCCGACGCGCCCGTGTATGAAGAACAAAGCGCGCGCTGGG 424
 Db 438 TCTTTGTATCCAAATTTTCTGCTGATGGCCCGCTGATGAAGAACAAATCAGAAGNATGGG 497
 QY 425 AGCCGACGACGAGGTGGTGTACCCCGAGAACCGCGTGTGTGCGCGCCGGAACGTGATGG 484
 Db 498 AGCCATGCACATGAGTGGTGTATCCAGATAATGGTGTCCTGTGTGACGCTAATGTGATGG 557
 QY 485 CCCTGAAGGTGGCGACCGGACCTGTATCTTGCACACACTACACCACTACCGGACGACAGA 544
 Db 558 CCCTTAAAGTCGGTGATCGTCTGTTGTATCTGCATCTCTATATCTTTACAGGTCGAAGA 617
 QY 545 AGGCGGTGGCGCCCTGACCAATGCCGCGCTTCCACTTTACCGGACATCCCGGCTCCAGATGC 604

Db 618 AAGAGTCGCTGCTTGCATATGCAGGATTTTCATTTTACAGACATCCGCTTCAGATGC 677
 QY 605 TCGGGAAGAAGACGAGTACTTCGAGCTGTACGAGGCGAGCGTGGCCCGGTACAGCG 664
 Db 678 CGAGGAAACGAAAGACGAGTACTTTGAACCTGTACGAGCATCTGTGGCTAGGTACAGT 737
 QY 665 ACCTGCCCGAGAGCCCAACTGA 687
 Db 738 ATCTTCCTGAAAGCAAAATGA 760

RESULT 13
 AX527912
 LOCUS AX527912
 DEFINITION Sequence 25 from Patent WO0230965.
 ACCESSION AX527912
 VERSION AX527912.1 GI:25172357
 KEYWORDS Heteractis crisp (leathery sea anemone)
 SOURCE Heteractis crisp
 ORGANISM Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Stichodactylidae; Heteractis.

REFERENCE
 1. Lukyanov, S.A., Fradkov, A.F., Lukyanov, K.A. and Gurskaya, N.G.
 Nucleic acids encoding stichodactylidae chromoproteins
 Patent: WO 0230965-A 25 18-APR-2002;
 Clontech Laboratories Inc. (US)

FEATURES
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 VERSION AY233273.1 GI:28629492
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 699)
 AUTHORS Chudakov, D.M., Belousov, V.V., Zaraisky, A.G., Novoselov, V.V., Staroverov, D.B., Zorov, D.B., Lukyanov, S. and Lukyanov, K.A.
 Kindling fluorescent proteins for precise in vivo photolabeling
 Nat. Biotechnol. 21 (2), 191-194 (2003)

FEATURES
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